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OM protein - protein search, using sw model

Run on: October 27, 2003, 19:11:58; Search time 33.6197 Seconds

(without alignments)

1902.657 Million cell updates/sec

Title: US-10-017-372E-33

Perfect score: 2139

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03:*

22:

23:

24:

1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:* 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:* 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:* /SIDS1/gcgdata/geneseg/genesegp-emb1/AA1984.DAT:* 6 : /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:* 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:* 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:* 10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:* 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:* 12: 13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:* 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:* 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:* 16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:* 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:* 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997 DAT: * 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:* 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* 21: /SIDS1/qcqdata/qeneseq/qeneseqp-emb1/AA2000.DAT: *

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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

		ક			202	
Result		Query				
No.	Score		Length	DB	ID	Description
				- - :		Description
1	2050.5	95.9	390	23	AAE13596	Porcine transformi
2	1928.5	90.2	390	22	AAM39186	Human polypeptide
3	1921.5	89.8	390	7	AAP61468	PreTGF-beta gene p
4	1921.5	89.8	390	11	AAR04034	Sequence of pre-TG
5	1921.5	89.8	390	11	AAR05258	Human pre-transfor
6	1921.5	89.8	390	12	AAR13813	Human pro-TGF-beta
7	1921.5	89.8	390	16	AAR73596	Human TGF-beta 1 p
8	1921.5	89.8	390	17	AAR90827	Pre-transforming g
9	1918.5	89.7	390	23	AAU77101	Human transforming
10	1918.5	89.7	390	23	AAE16943	Human transforming
11	1918	89.7	391	24	ABB82780	TGFB1 Arg25Pro pol
12	1916.5	89.6	390	13	AAR20124	Sequence of simian
13	1912.5	89.4	390	15	AAR46227	Human pre-TGF-beta
14	1911	89.3	391	16	AAR83054	Transforming growt
15	1910.5	89.3	390	19	AAW78785	Human pre-transfor
16	1909.5	89.3	390	22	AAB84601	Nucleotide sequenc
17	1907	89.2	391	9	AAP81362	Human transforming
18	1906	89.1	434	11	AAR03743	Monkey transformin
19	1902.5	88.9	390	24	ABB82781	TGFB1 Arg25Pro pol
20	1885.5	88.1	386	11	AAR05663	Simian Transformin
21	1880	87.9	387	11	AAR05664	Simian Transformin
22	1869.5	87.4	390	11	AAR05492	Chimeric simian TG
23	1865.5	87.2	390	13	AAR27522	TGF-beta 1/beta 2
24	1846	86.3	389	13	AAR29657	TGF-beta 1. Homo
25	1841	86.1	453	22	AAM40972	Human polypeptide
26	1760.5	82.3	390	13	AAR20126	Sequence of hybrid
27	1759.5	82.3	390	11	AAR05749	Human TGF-Beta2 ex
28	1753.5	82.0	390	11	AAR05665	Human Transforming
29	1751.5	81.9	390	11	AAR05666	Hybrid transformin
30	1744	81.5	391	10	AAP91900	Sequence encoded b
31	1716	80.2	389	16	AAR79921	Simian-human hybri
32	1300	60.8	278	15	AAR53090	Polypeptide cross-
33	1295	60.5	278	12	AAR12541	Latency associated
34	1262.5	59.0	458	23	ABG31507	LAP-mIFNB construc
35	1262.5	59.0	463	23	ABG31510	LAP-huIFNB constru
36	1171	54.7	290	22	ABG06792	Novel human diagno
37	1135	53.1	450	23	ABG31508	mIFNB-LAP construc
38	1118	52.3	448	23	ABG31509	huIFNB-LAP constru
39	944	44.1	227	22	ABG20234	Novel human diagno
40	903	42.2	236	22	ABG20233	Novel human diagno
41	870.5	40.7	382	21	AAB08338	Amino acid sequenc
42	870.5	40.7	382	23	AAU77105	Frog transforming
43	834.5	39.0	456	19	AAW78786	Pig transforming g
44	833.5	39.0	412	16	AAR73598	Human TGF-beta 3 p
45	829.5	38.8	412	13	AAR20621	Transforming Growt

```
RESULT 1
AAE13596
ΙD
     AAE13596 standard; Protein; 390 AA.
XX
AC
    AAE13596;
XX
DT
     26-FEB-2002 (first entry)
XX
DE
     Porcine transforming growth factor beta 1 (TGF-beta1) mutant.
XX
KW
     Porcine; transforming growth factor beta 1; TGF-betal; gene therapy;
KW
     IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
     multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW
KW
     diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;
KW
     mutein.
XX
OS
     Sus scrofa.
XX
FΗ
     Kev
                     Location/Qualifiers
FT
    Misc-difference 223
FT
                     /note= "Wild type Cys substituted with Ser"
FT
     Misc-difference 225
FT
                     /note= "Wild type Cys substituted with Ser"
XX
PN
     WO200181404-A2.
XX
PD
     01-NOV-2001.
XX
PF
     20-APR-2001; 2001WO-US12980.
XX
     20-APR-2000; 2000US-199014P.
PR
XX
PA
     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
ΡI
     Strober W, Nakamura K, Kitani A, Fuss IJ;
XX
DR
    WPI; 2002-026155/03.
DR
    N-PSDB; AAD22696.
XX
PT
     Composition for treating autoimmune diseases e.g. inflammatory bowel
PT
     disease in humans, comprises vector containing transforming growth
PT
     factor-beta under the control of inducible promoter -
XX
PS
     Example 1; Fig 1; 78pp; English.
XX
CC
     The invention relates to a composition containing a vector comprising a
CC
     gene encoding a regulatory transcription factor under the control of a
CC
     promoter encoding a transforming growth factor-beta (TGF-beta). The
CC
    vector is useful for expressing TGF-beta, such as TGF-betal, TGF-beta2
CC
     or TGF-beta3, its variants or homologues, by transfecting a cell which
CC
     is part of a host suspected of having an autoimmune disease, especially
CC
     inflammatory bowel disease (IBD), under conditions such that the
CC
     polypeptide encoded by the nucleic acid sequence in the vector is
CC
     expressed. The vector is delivered using a delivery system. The delivery
     of the vector results in substantial elimination of symptoms of the
CC
CC
     autoimmune disease and increased production of IL-10 by the host. The
CC
     composition is useful for treating various diseases with an autoimmune
```

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CC
    component such as multiple sclerosis, rheumatoid arthritis, systemic
CC
    lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC
    and psoriasis, and also for assaying the expression of a gene in a cell.
CC
    The vector is further useful for screening of the effect of test
    compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC
CC
    The present sequence is porcine TGF-betal mutant.
XX
SQ
             390 AA;
    Sequence
 Query Match
                      95.9%; Score 2050.5; DB 23; Length 390;
                      96.8%; Pred. No. 7.6e-176;
 Best Local Similarity
                          0; Mismatches
 Matches 390; Conservative
                                           0; Indels
                                                      13; Gaps
                                                                 1:
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Qу
            1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
Db
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Qу
            121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
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Db
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Qу
            111111111
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----
Db
                                                 -----ALDTNYCFS 287
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Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
QУ
            Db
        348 PGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
RESULT 2
AAM39186
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ID
XX
AC
    AAM39186;
XX
DT
    22-OCT-2001 (first entry)
XX
DE
    Human polypeptide SEQ ID NO 2331.
XX
KW
    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW
    peripheral nervous system; neuropathy; central nervous system; CNS;
    Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW
KW
    amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW
    chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
```

```
KW
     leukaemia.
XX
OS
    Homo sapiens.
XX
PN
    WO200153312-A1.
XX
PD
     26-JUL-2001.
ХX
PF
     26-DEC-2000; 2000WO-US34263.
XX
     21-JAN-2000; 2000US-0488725.
PR
     25-APR-2000; 2000US-0552317.
PR
     09-JUL-2000; 2000US-0598042.
PR
PR
     19-JUL-2000; 2000US-0620312.
PR
     03-AUG-2000; 2000US-0653450.
     14-SEP-2000; 2000US-0662191.
PR
PR
     19-OCT-2000: 2000US-0693036.
     29-NOV-2000; 2000US-0727344.
PR
XX
PΑ
     (HYSE-) HYSEQ INC.
XX
     Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PΙ
     Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y,
PΙ
                                                            Zhang J;
PΙ
     Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
     WPI; 2001-442253/47.
DR
     N-PSDB; AAI58342.
DR
XX
     Novel nucleic acids and polypeptides, useful for treating disorders
PT
PΤ
     such as central nervous system injuries -
XX
PS
     Example 4; SEQ ID NO 2331; 10078pp; English.
XX
CC
     The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC
     the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC
     immunosuppressant and cytostatic activity. The polynucleotides are useful
CC
     in gene therapy. A composition containing a polypeptide or polynucleotide
     of the invention may be used to treat diseases of the peripheral nervous
CC
CC
     system, such as peripheral nervous injuries, peripheral neuropathy and
CC
     localised neuropathies and central nervous system diseases, such as
CC
     Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC
     lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC
     utilisation of the activities such as: Immune system suppression,
CC
     Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC
     and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC
     assays for receptor activity, arthritis and inflammation, leukaemias and
CC
     C.N.S disorders.
CC
     Note: The sequence data for this patent did not form part of the printed
CC
     specification.
XX
SQ
     Sequence
               390 AA;
                          90.2%; Score 1928.5; DB 22; Length 390;
  Query Match
  Best Local Similarity
                          90.8%; Pred. No. 7.2e-165;
  Matches 366; Conservative 10; Mismatches
                                                  14; Indels
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QУ

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Db
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Qу
           Db
        61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
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Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
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Qу
           Db
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QУ
           Db
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Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
           Dh
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RESULT 3
AAP61468
ID
    AAP61468 standard; Protein; 390 AA.
XX
AC
    AAP61468;
XX
DT
    31-OCT-2002
              (updated)
DT
    28-OCT-1991
             (first entry)
XX
DE
    PreTGF-beta gene product.
XX
KW
    Transforming growth factor beta; cancer; wound healing.
XX
OS
    Unidentified.
XX
FΗ
    Key
                Location/Qualifiers
FT
    Protein
                279..390
XX
PN
    EP200341-A.
XX
PD
    10-DEC-1986.
XX
PF
    21-MAR-1986;
               86EP-0302112.
XX
PR
    22-MAR-1985;
               85US-0715142.
PR
    13-MAR-1987;
               87US-0025423.
XX
PA
    (GETH ) GENENTECH INC.
XX
```

```
Derynck RMA;
ΡI
XX
DR
    WPI; 1986-326875/50.
    N-PSDB; AAN60972.
DR
XX
PT
    TGF-beta prodn. from transformed hosts - useful esp. for treating
    wounds (J6 2/9/86).
PT
XX
PS
    Disclosure; Fig 1b; 26pp; English.
XX
CC
    The gene product is known to stimulate cell proliferation and
CC
    inhibit anchorage-dependent growth of a variety of human cancer cell
    lines, it is esp. useful in treatment of burns and the promotion of
CC
CC
    surface and internal wound healing. TGF-beta may be expressed from a
CC
    transformed CHO cell line.
    (Updated on 31-OCT-2002 to add missing OS field.)
CC
XX
SO
    Sequence
             390 AA;
 Query Match
                     89.8%; Score 1921.5; DB 7; Length 390;
                     90.6%; Pred. No. 3.1e-164;
 Best Local Similarity
 Matches 365; Conservative 10; Mismatches
                                         15; Indels
                                                                1;
                                                     13: Gaps
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Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qy
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Dh
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Qу
            121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKKVEOHVELYOKYSNNSWR 180
Db
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Qу
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        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----
Db
                                                  ----ALDTNYCFS 287
Qу
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 360
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Qy
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Db
RESULT 4
AAR04034
    AAR04034 standard; protein; 390 AA.
ID
XX
AC
    AAR04034;
```

```
DT
    25-MAR-2003
                 (updated)
DT
    31-OCT-2002
                 (updated)
DT
    31-MAY-1989
                 (first entry)
XX
DE
    Sequence of pre-TGF-beta 1.
XX
    Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW
KW
    inhibition.
XX
OS
    Homo sapiens.
XX
FH
                   Location/Qualifiers
    Key
FT
    CDS
                   348..500
XX
PN
    WO8912101-A.
XX
PD
    14-DEC-1989.
XX
PF
    08-JUN-1988;
                  88WO-US01945.
XX
                  88WO-US01945.
PR
    08-JUN-1988;
XX
PA
     (GETH ) GENENTECH INC.
XX
    Dernyck RMA, Goeddel DV;
PΙ
XX
DR
    WPI; 1990-007474/01.
DR
    N-PSDB; AAQ02815.
XX
    Nucleotide sequence encoding transforming growth factor beta-3 used as a
PT
    probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PT
PT
    and neoplastic cells, eg A549.
XX
PS
    Disclosure; Fig. 2; 61pp; English.
XX
    Sequence is an exon of transforming growth factor-beta 1 (pre-TGF-beta
CC
    1) polypeptide and corresponds to AA's 288-338 of mature TGF-beta 1. The
CC
    nucleic acid encoding second subtype of TGF-beta (TGF-beta 3) is useful
CC
CC
    as a probe or to produce TGF-beta 3 for inhibition of normal and
CC
    neoplastic cell growth.
CC
     (Updated on 31-OCT-2002 to add missing OS field.)
CC
     (Updated on 25-MAR-2003 to correct PR field.)
CC
     (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ
    Sequence
               390 AA;
  Query Match
                        89.8%; Score 1921.5; DB 11; Length 390;
  Best Local Similarity
                        90.6%; Pred. No. 3.1e-164;
                                              15; Indels
                                                            13; Gaps
  Matches 365; Conservative 10; Mismatches
                                                                         1;
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
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Db
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Qу
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XX

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XX
AC
    AAR05258;
XX
DT
    25-MAR-2003 (updated)
DT
    05-AUG-1990 (first entry)
XX
DE
    Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
XX
KW
    Transforming growth factor-beta-1 (TGF-beta-1);
KW
    neoplastic cell line inhibition;
KW
    EGF-potentiated anchorage-independent growth.
XX
OS
    Homo sapiens.
XX
FΗ
                  Location/Oualifiers
    Kev
FT
    Peptide
                  1..278
FT
                  279..2011
    Protein
FT
    Domain
FT
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FT
    Modified-site
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FT
                  /note="potential N-glycosylation site "
FT
    Modified-site
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                  /note="as above"
    Modified-site
FT
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FT
                  /note="as above"
FT
    Cleavage-site
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                  /note="proteolytic cleavage site"
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PN
    US4886747-A.
XX
PD
    12-DEC-1989.
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61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120

Db

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XX
PF
    13-MAR-1987:
                87US-0025423.
XX
PR
    13-MAR-1987;
                 87US-0025423.
                 85US-0715142.
PR
    22-MAR-1985;
XX
    (GETH ) GENENTECH INC.
PA
XX
    Derynck RMA, Goeddel DV;
ΡI
XX
DR
    WPI; 1990-051338/07.
    N-PSDB; AAQ93301.
DR
XX
PT
    Nucleic acid encoding transforming growth factor-beta -
    cloned into expression vectors for expression in eukaryotic host
PT
PT
    cells for therapeutic use
XX
PS
    Disclosure; Fig 1b; 28pp; English.
XX
CC
    Pre-TGF-beta-1 is a polypeptide of 390 amino acids. Post-transitional
CC
    cleavage of the precursor gives rise to the mature TGF-beta monomer.
CC
    The sequence for human TGF-beta was determined by direct amino acid
CC
    sequence analysis and by deduction from the TGF-beta cDNA. It is
    capable of inducing EGF-potentiated anchorage-independent growth of
CC
    target cell lines, and/or growth inhibition of neoplastic cell lines.
CC
    can be used for treating wounds, eg burns or epidermal ulcers.
CC
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence
             390 AA;
                      89.8%; Score 1921.5; DB 11; Length 390;
 Query Match
 Best Local Similarity
                      90.6%; Pred. No. 3.1e-164;
 Matches 365; Conservative 10; Mismatches
                                         15; Indels
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
            11111111
        241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----
Db
                                                   -----ALDTNYCFS 287
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
```

```
Qy
          361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
              Dh
          348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 6
AAR13813
ID
    AAR13813 standard; Protein; 390 AA.
XX
AC
    AAR13813;
XX
DT
    20-NOV-1991 (first entry)
XX
DE
    Human pro-TGF-beta 1.
XX
KW
    Osteogenetic; tumoricidal.
XX
OS
    Homo sapiens.
XX
FΗ
    Key
                    Location/Qualifiers
FT
    Peptide
FT
                    /note= "signal peptide"
FT
    Peptide
                    30..390
FT
                    /note= "pro-TGF-beta 1"
FT
    Peptide
                    279..390
FT
                    /note= "TGF-beta 1"
XX
ΡN
    JP03180192-A.
XX
PD
    06-AUG-1991.
XX
PF
    07-DEC-1989;
                  89JP-0318243.
XX
PR
    07-DEC-1989;
                   89JP-0318243.
XX
PA
     (KIRI ) KIRIN BREWERY KK.
XX
DR
    WPI; 1991-271579/37.
DR
    N-PSDB; AAQ13392.
XX
PT
    Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
PT
    preparing DNA chain contg. base sequence coding for human
PT
    pre:pro-TGF-beta 1, forming expression vector etc.
XX
PS
    Claim 1; Fig 1; 16pp; Japanese.
XX
CC
    The amino acid sequence codes for human prepro-TGF-beta 1 which
CC
    can be produced by recombinant methods, it has osteogenetic and
CC
    tumoricidal activity.
XX
SO
    Sequence
               390 AA;
 Query Match
                         89.8%; Score 1921.5; DB 12; Length 390;
 Best Local Similarity
                         90.6%; Pred. No. 3.1e-164;
 Matches 365; Conservative 10; Mismatches
                                               15; Indels
                                                              13; Gaps
                                                                           1;
```

```
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
           Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
           Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
QУ
           288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
           Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 7
AAR73596
TD
    AAR73596 standard; Protein; 390 AA.
XX
AC
   AAR73596;
XX
DT
    25-MAR-2003
              (updated)
DT
    20-DEC-1995
              (first entry)
XX
DE
   Human TGF-beta 1 protein.
XX
KW
    Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;
KW
    TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
KW
    bone-inducing cofactor.
XX
OS
   Homo sapiens.
XX
PN
   US5409896-A.
XX
PD
    25-APR-1995.
XX
PF
    12-NOV-1993;
                93US-0132405.
XX
PR
    01-SEP-1989;
               89US-0401906.
PR
    12-NOV-1991;
                91US-0790856.
PR
    18-MAY-1993;
                93US-0063841.
PR
    12-NOV-1993;
                93US-0132405.
XX
```

```
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Ammann AJ. Rudman CG:
XX
DR
    WPI; 1995-169610/22.
XX
    Compsn. for treating skeletal tissue deficiency - comprising
PT
PΤ
    transforming growth factor-beta and an osteogenic cell source in a
PT
    carrier
XX
PS
    Claim 3; Column 15-18; 19pp; English.
XX
CC
    This sequence represents human transforming growth factor-beta 1
CC
    (TGF-beta 1). This sequence and the sequence for human TGF-beta 3 (see
    AAR73598) are claimed within the scope of the invention. The invention
CC
CC
    is a composition consisting of a TGF-beta protein and an osteogenic cell
CC
    source (OCS) formulated in an acceptable carrier other than a bone
CC
    morphogenic cofactor. This composition can be used for the restoration
CC
    of bone deficiency. This provides for the generation of mature bone
CC
    only where it is required, without the inclusion of a specific
CC
    bone-inducing cofactor. This method can be used with any of the 5 human
    TGF-beta's or with TGF-beta from other species.
CC
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence
             390 AA;
 Query Match 89.8%; Score 1921.5; DB 16; Length 390; Best Local Similarity 90.6%; Pred. No. 3.1e-164;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                       13; Gaps
                                                                  1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
QУ
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
Qу
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLOVDINGFT 240
Dh
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
QУ
            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            348 PGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
Db
```

```
RESULT 8
AAR90827
ID
     AAR90827 standard; Protein; 390 AA.
XX
AC
     AAR90827;
XX
DT
     25-MAR-2003
                   (updated)
DT
     25-JAN-1980
                  (first entry)
XX
DE
     Pre-transforming growth factor beta 1.
XX
KW
     transforming growth factor beta 1; wound healing;
KW
     recombinant production.
XX
OS
     Homo sapiens.
XX
FH
                     Location/Oualifiers
     Key
FT
     Domain
                     8..23
FT
                     /note= "hydrophobic domain"
FT
     Modified-site
                     82..84
FT
                     /note= "potential N-glycosylation site"
FT
     Modified-site
                     136..138
FT
                     /note= "potential N-glycosylation site"
FT
     Modified-site
                     176..178
FT
                     /note= "potential N-glycosylation site"
FT
     Cleavage-site
                     277..279
FT
                      /note= "trypsin-like peptidase cleavage site"
FT
     Protein
                     279..390
FT
                     /label= mature_TGF_beta_1
XX
PN
     US5482851-A.
XX
PD
     09-JAN-1996.
XX
PF
     05-NOV-1993;
                   93US-0147364.
XX
PR
     13-MAR-1987;
                    87US-0025423.
PR
     22-MAR-1985;
                    85US-0715142.
PR
     04-AUG-1989;
                    89US-0389929.
                    92US-0845893.
PR
     04-MAR-1992;
PR
     05-NOV-1993;
                    93US-0147364.
XX
PA
     (GETH ) GENENTECH INC.
XX
PΙ
     Derynck RMA, Goeddel DV;
XX
DR
    WPI; 1996-076891/08.
DR
    N-PSDB; AAT15720.
XX
PT
     New recombinant human transforming growth factor-beta prods. - produced
PΤ
     using Chinese hamster ovary cells, for use in diagnostic applications
PT
     or in therapy
XX
PS
     Example 3; Fig 1A-C; 26pp; English.
XX
```

```
CC
    by AAT15720. The mature TGF beta 1 monomer is cleaved from the
CC
    precursor at the Arg-Arg dipeptide immediately preceding the mature
CC
    TGF-beta 1 NH2-terminus. It does not contain a recognisable N-terminal
CC
    signal peptide typical of most secreted proteins. The pre-TGF beta 1
CC
    contains several pairs of basic residues which could undergo
CC
    post-translational cleavage and give rise to separate polypeptide
CC
    entities. The precursor contains 3 potential N-glycosylation sites, none
CC
    of which are localised in the mature TGF beta 1. This is useful in
CC
    purification of the mature protein. TGF beta 1 can be used in, e.g. wound
CC
    healing.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
             390 AA;
SO
    Sequence
 Query Match
                     89.8%; Score 1921.5; DB 17; Length 390;
 Best Local Similarity 90.6%; Pred. No. 3.1e-164;
 Matches 365; Conservative 10; Mismatches 15; Indels
                                                     13; Gaps
                                                                1:
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Dh
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
QУ
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
            241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLQSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHN 360
Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 347
Db
Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
            Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
RESULT 9
AAU77101
    AAU77101 standard; Protein; 390 AA.
XX
AC
    AAU77101;
XX
DT
    05-JUN-2002 (first entry)
XX
    Human transforming growth factor beta 1 (TFG-beta-1) polypeptide.
DE
```

The pre-transforming growth factor (TGF) beta 1 protein is encoded

CC

```
XX
KW
     Human; transforming growth factor beta; TGF-beta; insulin production;
KW
     type I diabetes mellitus; pancreatic cell outgrowth; wound healing;
KW
     pancreatic duct tissue; ischaemia; stroke; nervous system aging;
KW
     neurological condition; neurodegenerative disease; inflammation;
     vasal injury; chemical injury; traumatic injury; tumour-induced injury;
KW
KW
     amyotrophic lateral sclerosis; spinocerebellar degeneration;
KW
     immunological disease; multiple sclerosis; TGF-beta-1.
XX
OS
     Homo sapiens.
XX
ΡN
     WO200212336-A2.
XX
PD
     14-FEB-2002.
XX
PF
     09-FEB-2001; 2001WO-US04192.
XX
PR
     09-AUG-2000; 2000US-0635368.
XX
PA
     (CURI-) CURIS INC.
XX
PΙ
     Wang M, Pang K;
XX
DR
     WPI; 2002-257468/30.
XX
PT
     Treating a subject with a disorder resulting from insufficient insulin
PT
     production, and inducing outgrowth of pancreatic cells, involves using
PT
     a transforming growth factor beta therapeutic
XX
PS
     Disclosure; Fig 1; 77pp; English.
XX
CC
     The invention relates to treating a subject with a disorder resulting
CC
     from insufficient insulin production, involving contacting the subject
CC
     with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta
CC
     polypeptides can be used for treating a subject with a disorder resulting
CC
     from insufficient insulin production, e.g. type I diabetes mellitus, and
CC
     for inducing outgrowth of pancreatic cells associated with pancreatic
CC
     duct tissue within a subject. A composition comprising a TGF-beta protein
CC
     may be useful in wound healing and treatment of neurological conditions
CC
     derived from acute, subacute or chronic injury to the nervous system,
CC
     including traumatic injury, chemical injury, vasal injury and deficits
CC
     (such as ischaemia resulting from stroke), together with
CC
     infectious/inflammatory and tumour-induced injury, aging of the nervous
CC
     system including Alzheimer's disease, chronic neurodegenerative diseases
CC
     including Parkinson's disease, Huntington's chorea, amyotrophic lateral
     sclerosis, spinocerebellar degenerations and chronic immunological
CC
CC
     diseases of the nervous system or affecting the nervous system, including
CC
     multiple sclerosis. This sequence represents the human TGF-beta-1
CC
     protein.
ХX
SQ
     Sequence
                390 AA;
  Query Match
                          89.7%; Score 1918.5; DB 23; Length 390;
  Best Local Similarity
                          90.6%;
                                  Pred. No. 5.7e-164;
  Matches 365; Conservative 10; Mismatches
                                                  15; Indels
                                                                13; Gaps
                                                                             1;
```

QУ

```
Db
          1 MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
QУ
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
            Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR----
                                                  ----- ALDTNYCFS 287
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 360
Qу
            Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 347
Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
            348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Dh
RESULT 10
AAE16943
ID
    AAE16943 standard; Protein; 390 AA.
XX
AC
    AAE16943;
XX
DT
    18-APR-2002 (first entry)
XX
DE
    Human transforming growth factor-betal (TGF-betal) protein.
XX
KW
    Human; transforming growth factor-betal; TGF-betal; osteoporosis;
KW
    latency associated peptide; LAP; integrin alphavbeta3; apoptosis;
KW
    immunomodulation; inflammatory disease; fibrotic disease; cancer;
ΚW
    diabetic retinopathy; chronic obstructive pulmonary disorder;
KW
    bone resorption; rheumatoid arthritis; psoriasis; restenosis;
KW
    atherosclerosis; liver fibrosis; asthma; cytostatic; osteopathic;
KW
    ophthalmological; antiarteriosclerotic; vasotropic.
XX
OS
    Homo sapiens.
XX
FΗ
    Key
                  Location/Qualifiers
FT
    Peptide
                  1..29
FT
                  /label= Signal peptide
FΤ
                  30.,278
    Region
FT
                  /note= "LAP-betal"
FT
    Domain
                  244..246
FΤ
                  /note= "RGD motif"
FT
    Protein
                  279..390
FT
                  /note= "Human mature TGF-betal protein"
```

```
XX
PN
    WO200190186-A1.
XX
PD
    29-NOV-2001.
XX
PF
    25-MAY-2001; 2001WO-GB02352.
XX
PR
    26-MAY-2000; 2000GB-0012991.
PR
    05-JAN-2001; 2001GB-0000286.
XX
PA
    (GLAX ) GLAXO GROUP LTD.
XX
PΙ
    Ludbrook S, Barry S, Horgan C, Miller D;
XX
DR
    WPI; 2002-097645/13.
XX
PT
    Identifying modulators of interactions between latency associated
PT
    peptides and integrin alphavbeta3 for therapeutics, by contacting the
PT
    peptide and integrin with a test product and determining if the product
PT
    modulates interaction -
XX
PS
    Disclosure; Page 37-39; 44pp; English.
XX
CC
    The invention relates to a method for identification of a modulator
CC
    of the interaction between latency associated peptide (LAP) of
CC
    transforming growth factor-betal (TGF-betal) and integrin alphavbeta3.
CC
    The method is useful for identifying a modulator of the interaction
CC
    between LAP and integrin alphavbeta3. The method is useful for
CC
    immunomodulation, in the treatment of inflammatory disease, fibrotic
CC
    disease, cancer, diabetic retinopathy, bone resorption or osteoporosis,
CC
    and for preventing apoptosis administering the modulator to the host.
CC
    The modulator (inhibitor of the interaction between LAP-betal and
CC
    integrin alphavbeta3) is useful in the manufacture of a medicament for
CC
    immunomodulation. The modulator (activator of the interaction between
CC
    LAP-betal and integrin alphavbeta3 ) is useful in the manufacture of
CC
    medicament for preventing apoptosis. The modulator is useful for
CC
    treating a inflammatory or fibrotic disease such as chronic obstructive
CC
    pulmonary disorder, rheumatoid arthritis, psoriasis, restenosis,
CC
    atherosclerosis, liver fibrosis and asthma. The present sequence is
CC
    human TGF-betal protein.
XX
SO
    Sequence
              390 AA;
 Query Match
                        89.7%; Score 1918.5; DB 23; Length 390;
 Best Local Similarity
                        90.6%; Pred. No. 5.7e-164;
 Matches 365; Conservative 10; Mismatches
                                             15; Indels
                                                           13; Gaps
                                                                        1;
Qу
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
             Db
           1 MPPSGLRLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
             Db
          61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYOKYSNDSWR 180
Qу
```

```
Db
         121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
             Db
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
             11111111
Dh
         241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
         301 STEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 360
QУ
             Db
         288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
         361 PGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
Qу
             Dh
         348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 11
ABB82780
ΙD
    ABB82780 standard; Protein; 391 AA.
XX
AC
    ABB82780;
XX
DT
    18-MAR-2003 (first entry)
XX
DE
    TGFB1 Arg25Pro polymorphism G-allele protein sequence.
XX
    Polymorphism; transforming growth factor beta 1; TGFB1; TGFbeta-1;
KW
KW
    renal failure; nephrotropic; human; allele.
XX
OS
    Homo sapiens.
XX
ΡN
    WO200290585-A2.
XX
PD
    14-NOV-2002.
XX
ΡF
    08-MAY-2002; 2002WO-GB02066.
XX
    09-MAY-2001; 2001GB-0011277.
PR
XX
    (UYSH-) UNIV SHEFFIELD HALLAM.
PA
XX
PΙ
    El-Nahas AM, Blakemore A, Khalil MS;
XX
DR
    WPI; 2003-120560/11.
DR
    N-PSDB; ABV75391.
XX
PТ
    Determining an individual's susceptibility to the progression of renal
PΤ
    failure comprises detecting the presence of a genetic polymorphism
PT
    pattern in transforming growth factor beta 1 (TGFB1) gene in a sample
PΤ
    from the individual
XX
PS
    Claim 51; Page 59-61; 62pp; English.
XX
CC
    The invention relates to determining an individual's susceptibility to
```

```
renal failure and invovles detecting the presence of a genetic
CC
    polymorphism pattern in transforming growth factor beta 1 (TGFB1) gene in
CC
    a sample from an individual, where polymorphism pattern is associated
CC
    with renal failure. The method is useful for determining an individual's
CC
    susceptibility to the progression of renal failure. The nucleic acid
CC
    comprising a T(-509)C polymorphism of TGFB1 gene, or a polypeptide
CC
    comprising a sequence of 391 amino acids is useful for preparing a
CC
    medicament for retarding or preventing the progression of renal disease,
CC
    and for drug research purposes for retarding or preventing the
    progression of renal disease. Sequences ABV75386-88 represents the
CC
CC
    protein sequence for the TGFB1 G-allele of the Arq25Pro polymorphism
CC
    of exon 1.
XX
SO
    Sequence
             391 AA;
 Query Match
                     89.7%; Score 1918; DB 24; Length 391;
 Best Local Similarity
                     90.6%; Pred. No. 6.4e-164;
 Matches 366; Conservative 10; Mismatches 14; Indels
                                                      14; Gaps
                                                                 2;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Db
          1 MPPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Dh
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
Db
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
            181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Db
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCF 299
Qу
             241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCF 287
Db
        300 SSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQH 359
QУ
            288 SSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQH 347
Db
Qy
        360 NPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
            Db
        348 NPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
RESULT 12
AAR20124
    AAR20124 standard; Protein; 390 AA.
ID
XX
AC
    AAR20124;
XX
DT
    25-MAR-2003 (updated)
DT
    16-APR-1992 (first entry)
XX
```

CC

```
Sequence of simian transforming growth factor (TGF) beta-1.
DE
XX
KW
    Hypertension therapy; hypotensive agent; blood pressure modulator.
XX
OS
    Monkey.
XX
FΗ
                   Location/Qualifiers
    Key
FT
    Peptide
                   8..21
FT
    Protein
                   279..390
ХΧ
PN
    WO9119513-A.
XX
PD
    26-DEC-1991.
XX
ΡF
    20-JUN-1991; 91WO-US04449.
XX
PR
    20-JUN-1990; 90US-0541221.
XX
PA
    (BRIM ) BRISTOL-MYERS SOUIBB CO.
XX
PΙ
    Oleson FB, Comereski CR;
XX
DR
    WPI: 1992-024199/03.
DR
    N-PSDB; AAQ20289.
XX
PT
    Use of transforming growth factor (TGF)-beta and their
PT
    antagonists - for modulating blood pressure, for treating
PT
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
CC
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
    (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
    Sequence
SO
              390 AA;
 Query Match
                       89.6%; Score 1916.5; DB 13; Length 390;
 Best Local Similarity 90.3%; Pred. No. 8.7e-164;
 Matches 364; Conservative 10; Mismatches
                                            16; Indels
                                                          13; Gaps
                                                                     1;
Qу
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
             Db
          1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGQILSKLRLA 60
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
             Db
          61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
             Db
         121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEOHVELYOKYSNNSWR 180
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Qу
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
            181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Db
Qу
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
            Db
         241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
Qу
         301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
             Db
         288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Qу
         361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
             Db
         348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 13
AAR46227
ΙD
    AAR46227 standard; Protein; 390 AA.
XX
AC
    AAR46227;
XX
DT
    25-MAR-2003
                (updated)
DT
    09-JUL-1994 (first entry)
XX
DE
    Human pre-TGF-beta-1.
XX
KW
    TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW
    transforming growth factor beta-3; recombinant; wound healing;
KW
    vulnerary.
XX
OS
    Homo sapiens.
XX
FΗ
    Key
                  Location/Qualifiers
FT
    Peptide
                  279..390
FT
                  /label= Mat_peptide
FT
    Cleavage-site
                  279
FT
                  /note= "TGF-beta-1 release site"
FT
    Modified-site
                  82..84
FT
                  /label= N-glycosylation site
FT
    Modified-site
                  136..138
FT
                  /label= N-glycosylation_site
    Modified-site
FT
                  176..178
FT
                  /label= N-glycosylation site
XX
PN
    US5284763-A.
XX
PD
    08-FEB-1994.
XX
PF
    04-MAR-1992;
                 92US-0845893.
XX
PR
    22-MAR-1985;
                 85US-0715142.
PR
    13-MAR-1987;
                 87US-0025423.
PR
    04-AUG-1989;
                 89US-0389929.
PR
    04-MAR-1992;
                 92US-0845893.
```

```
XX
PΑ
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynk RMA, Goeddel DV;
XX
DR
    WPI; 1994-056343/07.
DR
    N-PSDB; AAQ56923.
XX
PT
    Nucleic acid sequences encoding transforming growth factor-beta -
PT
    diagnostic probes, and for use in therapeutics
XX
PS
    Disclosure; Fig 1b; 25pp; English.
XX
CC
    cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC
    pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC
    corresponding amino acid sequences were determined (AAR46227-29,
CC
    respectively). A genomic fragment corresponding to a human TGF-
CC
    beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC
    determined (AAR46230). The sequences have been used in the
CC
    construction of vectors for the expression of recombinant TGF-
CC
    beta.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ
    Sequence
             390 AA;
 Query Match
                     89.4%; Score 1912.5; DB 15; Length 390;
 Best Local Similarity 90.3%; Pred. No. 2e-163;
 Matches 364; Conservative 10; Mismatches
                                        16; Indels
                                                     13; Gaps
                                                                1:
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Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEREPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLOVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
            Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLOSSRHRR-----
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            348 PGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
Db
```

```
RESULT 14
AAR83054
    AAR83054 standard; Protein; 391 AA.
XX
AC
    AAR83054;
XX
DT
     25-JUN-1996 (first entry)
XX
DE
     Transforming growth factor-beta 1.
XX
     macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW
     interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW
    nitric oxide production; hypotension; inflammation; septic shock;
KW
KW
     treatment.
XX
OS
    Mammalian sp.
XX
                     Location/Qualifiers
FH
     Key
                     279..391
FT
     Protein
                     /note= "represents the mature active TGF beta-1 mol."
FT
XX
PN
    WO9526745-A1.
XX
PD
     12-OCT-1995.
XX
PF
     05-APR-1994;
                    94WO-US03705.
XX
     05-APR-1994;
                  94WO-US03705.
PR
XX
     (HARD ) HARVARD COLLEGE.
PA
XX
     Lee M, Perrella MA;
PΙ
XX
     WPI; 1995-358443/46.
DR
DR
     N-PSDB; AAT05876.
XX
     Treatment of hypotension, esp. in septic shock - by administering
PT
     transforming growth factor-beta e.g. to inhibit inducible nitric
PT
PT
     oxide synthase gene transcription
XX
PS
     Disclosure; Fig 17; 52pp; English.
XX
     Transforming growth factor-beta 1 (TGF-beta 1) has been found to inhibit
CC
     inducible nitric oxide synthase (iNOS) gene transcription, esp. in
CC
     interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at
CC
     a dose which does not inhibit consitutive NOS. TGF-beta 1 or 2
CC
CC
     (AAR83055) or their active fragments (esp. derived from the
CC
     carboxy-terminal 112 amino acids), can be used in the treatment of
CC
     hypotension, such as that associated with severe inflammation or septic
CC
     shock.
XX
SQ
     Sequence
                391 AA;
                          89.3%; Score 1911; DB 16; Length 391;
  Query Match
  Best Local Similarity
                          90.3%; Pred. No. 2.7e-163;
  Matches 365; Conservative 10; Mismatches
                                                 15; Indels
                                                                14; Gaps
```

```
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Dh
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQ1 120
Qу
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Dh
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
Dh
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
            111111111111
Db
        181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYCF 299
Qу
            241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTNYCF 287
Db
        300 SSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQH 359
Qу
            288 SSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQH 347
Db
        360 NPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            348 NPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
Db
RESULT 15
AAW78785
    AAW78785 standard; Protein; 390 AA.
ID
XX
AC
    AAW78785;
XX
DT
    25-MAR-2003
               (updated)
DT
    21-DEC-1998
               (first entry)
XX
DE
    Human pre-transforming growth factor-beta 1.
XX
KW
    Transforming growth factor-beta 1; TGF-beta 1; human.
XX
OS
    Homo sapiens.
XX
FH
                 Location/Qualifiers
    Key
FT
    Domain
FT
                 /note= "hydrophobic domain"
FT
    Protein
                 279..390
FT
                 /label= Mat protein
FΤ
    Modified-site
                 82..84
FT
                 /note= "Asn is N-glycosylated"
FT
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                 136..138
FT
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FT
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FT
                 277..278
    Cleavage-site
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XX
PN
    US5801231-A.
XX
PD
    01-SEP-1998.
XX
PF
    30-MAY-1995;
                 95US-0454468.
XX
PR
    13-MAR-1987;
                87US-0025423.
PR
    22-MAR-1985;
                85US-0715142.
PR
    04-AUG-1989;
                89US-0389929.
PR
    04-MAR-1992;
                92US-0845893.
PR
    05-NOV-1993;
                 93US-0147364.
PR
    30-MAY-1995;
                  95US-0454468.
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynck RMA, Goeddel DV;
XX
DR
    WPI: 1998-494840/42.
    N-PSDB; AAV52933.
DR
XX
PT
    DNA encoding transforming growth factor-beta precursor sequence -
    useful for analysis to perform manipulations to increase yield of
PT
PT
    recombinant production of the protein
XX
PS
    Example 3; Fig 1B 1-3; 26pp; English.
XX
CC
    This is the amino acid sequence of human transforming growth
CC
    factor-beta 1 precursor (preTGF-beta 1). It was deduced from
CC
    a preTGF-beta 1 cDNA sequence (see AAV52933). The invention relates
CC
    to the recombinant production of TGF-beta. Biologically active
CC
    TGF-beta is defined as being capable of inducing EGF-potentiated
CC
    anchorage independent growth of target cell lines and/or growth
CC
    inhibition of neoplastic cell lines. Nucleic acids encoding
CC
    TGF-beta have been isolated and cloned into vectors which are
CC
    replicated in bacteria and expressed in eukaryotic cells. TGF-beta
CC
    recovered from transformed cells is used in known therapeutic
CC
    applications.
    (Updated on 25-MAR-2003 to correct PF field.)
CC
XX
SO
    Sequence
              390 AA;
 Query Match
                       89.3%; Score 1910.5; DB 19; Length 390;
 Best Local Similarity 90.1%; Pred. No. 3e-163;
 Matches 363; Conservative 10; Mismatches
                                            17; Indels
                                                          13; Gaps
                                                                      1;
Qу
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
             1 MPPSGLRLLPLLLPLLWLLVLTPGPPAPGLSTCKTIDMEQVKRKRIEAIRGQILSKLRLA 60
Db
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
             61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
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/note= "cleavage site for relase of TGF-beta 1"

FT

Db	121	YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
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Db	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
Qу	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300:
Db	241	TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYCFS 287
Qу	301	STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Db	288	
Qу	361	PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Db	348	PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

Search completed: October 28, 2003, 09:06:48 Job time : 34.6197 secs

> GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 09:09:54; Search time 24.4507 Seconds

(without alignments)

2760.110 Million cell updates/sec

Title: US-10-017-372E-33

Perfect score: 2139

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

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    /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
11:
12:
    /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13:
    /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*
    /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*
14:
15: /cgn2 6/ptodata/2/pubpaa/US10C PUBCOMB.pep:*
16: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
    /cgn2 6/ptodata/2/pubpaa/US60 NEW PUB.pep: *
17:
    /cgn2 6/ptodata/2/pubpaa/US60 PUBCOMB.pep:*
18:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

૦

Result No.	Score	Query Match	Length	DB	ID	Description
1	2032.5	95.0	390	11	US-09-214-592-26	Sequence 26, Appl
2	1931.5	90.3	390	11	US-09-214-592-29	Sequence 29, Appl
3	1928.5	90.2	390	15	US-10-087-268-2	Sequence 2, Appli
4	1921.5	89.8	390	15	US-10-087-268-5	Sequence 5, Appli
5 6	1918.5	89.7	390	12	US-10-276-947-1	Sequence 1, Appli
	1916.5	89.6	390	11	US-09-214-592-33	Sequence 33, Appl
7	1911	89.3	391	11	US-09-214-592-17	Sequence 17, Appl
8	1907.5	89.2	390	10	US-09-756-283A-23	Sequence 23, Appl
9	1895.5	88.6	390	11	US-09-214-592-28	Sequence 28, Appl
10	1837.5	85.9	390	11	US-09-214-592-20	Sequence 20, Appl
11	1837.5	85.9	390	11	US-09-214-592-23	Sequence 23, Appl
12	1574.5	73.6	315	11	US-09-214-592-25	Sequence 25, Appl
13	1262.5	59.0	455	10	US-09-756-283A-20	Sequence 20, Appl
14	1139	53.2	447	10	US-09-756-283A-22	Sequence 22, Appl
15	1049	49.0	373	11	US-09-214-592-32	Sequence 32, Appl
16	873.5	40.8	412	11	US-09-214-592-31	Sequence 31, Appl
17	870.5	40.7	382	11	US-09-214-592-34	Sequence 34, Appl
18	870	40.7	383	10	US-09-756-283A-27	Sequence 27, Appl
19	836	39.1	409	11	US-09-214-592-27	Sequence 27, Appl
20	832.5	38.9	410	11	US-09-214-592-22	Sequence 22, Appl
21	831.5	38.9	412	11	US-09-214-592-24	Sequence 24, Appl
22	829.5	38.8	412	11	US-09-214-592-19	Sequence 19, Appl
23	829.5	38.8	412	14	US-10-028-158-21	Sequence 21, Appl
24	829	38.8	414	11	US-09-214-592-21	Sequence 21, Appl
25	825.5	38.6	412	10	US-09-756-283A-25	Sequence 25, Appl
26	814	38.1	414	10	US-09-756-283A-24	Sequence 24, Appl
27	814	38.1	414	11	US-09-214-592-18	Sequence 18, Appl
28	813	38.0	412	11	US-09-214-592-30	Sequence 30, Appl
29	794	37.1	304	10	US-09-756-283A-26	Sequence 26, Appl
30	755.5	35.3	139	14	US-10-002-278-8	Sequence 8, Appli
31	640	29.9	114	10	US-09-813-459-22	Sequence 22, Appl
32	640	29.9	114	14	US-10-115-406-21	Sequence 21, Appl
33	640	29.9	114	15	US-10-154-333-23	Sequence 23, Appl
34	640	29.9	115	10	US-09-859-211-47	Sequence 47, Appl
35	640	29.9	115	10	US-09-880-708-25	Sequence 25, Appl

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29.9
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36
      640
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37
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38
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                    112 10
                             US-09-813-271B-2
                                                        Sequence 13, Appl
                    113 10
                             US-09-813-398-13
39
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            29.8
                                                        Sequence 1, Appli
40
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                             US-10-187-394-1
                             US-10-115-406-24
                                                        Sequence 24, Appl
41
      542
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                             US-10-154-333-26
                                                        Sequence 26, Appl
42
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            25.0
                    112 10
                             US-09-813-271B-8
43
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                                                        Sequence 25, Appl
      505
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                   114 14
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44
                    114 15 US-10-154-333-27
                                                        Sequence 27, Appl
45
      505
            23.6
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ALIGNMENTS

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RESULT 1
US-09-214-592-26
; Sequence 26, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
 APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEO ID NOS: 34
  SOFTWARE:
; SEQ ID NO 26
   LENGTH: 390
   TYPE: PRT
   ORGANISM: porcine
US-09-214-592-26
                      95.0%; Score 2032.5; DB 11; Length 390;
 Query Match
 Best Local Similarity 95.8%; Pred. No. 1.4e-181;
 Matches 386; Conservative
                          1; Mismatches
                                           3; Indels
                                                      13; Gaps
                                                                 1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
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            Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMLESGNQI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
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Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
           Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRR--
                                                   --ALDTNYCFS 287
Qу
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
            Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            348 PGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
Db
RESULT 2
US-09-214-592-29
; Sequence 29, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
 SEQ ID NO 29
   LENGTH: 390
   TYPE: PRT
   ORGANISM: ovine
US-09-214-592-29
 Query Match
                     90.3%; Score 1931.5; DB 11; Length 390;
 Best Local Similarity 90.6%; Pred. No. 4e-172;
 Matches 365; Conservative 10; Mismatches
                                       15; Indels
                                                    13; Gaps
                                                              1;
QУ
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Dh
          1 MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKGIEAIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           61 SPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           Db
        121 YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREEIEGFRLSAHCSCDSKDNTLQVDINGFS 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
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Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRR------ALDTNYCFS 287
       301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
           288 STEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
           348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 3
US-10-087-268-2
; Sequence 2, Application US/10087268
; Publication No. US20030119010A1
: GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
 CURRENT APPLICATION NUMBER: US/10/087,268
 CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Human
US-10-087-268-2
 Query Match
                    90.2%; Score 1928.5; DB 15; Length 390;
 Best Local Similarity 90.8%; Pred. No. 7.6e-172;
 Matches 366; Conservative 10; Mismatches
                                                   13; Gaps
                                       14; Indels
                                                             1;
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
           1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
        61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
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           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
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Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYOKYSNDSWR 180
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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           181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
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        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
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Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
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           Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 4
US-10-087-268-5
; Sequence 5, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
  APPLICANT: Jonsonn, Julie Ruth
  APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
 FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
; SEO ID NO 5
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Human
US-10-087-268-5
 Query Match
                     89.8%; Score 1921.5; DB 15; Length 390;
 Best Local Similarity 90.6%; Pred. No. 3.4e-171;
 Matches 365; Conservative 10; Mismatches
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                                                    13; Gaps
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         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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           Db
         1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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         61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
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        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
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        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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           11111111
Db
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        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
           288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
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        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
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RESULT 5
US-10-276-947-1
; Sequence 1, Application US/10276947
; Publication No. US20030176315A1
; GENERAL INFORMATION:
  APPLICANT: GLAXO GROUP LIMITED
  TITLE OF INVENTION: MEDICAL PRODUCTS
  FILE REFERENCE: PG3949
  CURRENT APPLICATION NUMBER: US/10/276,947
  CURRENT FILING DATE: 2002-11-21
  PRIOR APPLICATION NUMBER: GB 0012991.6
  PRIOR FILING DATE: 2000-05-26
  PRIOR APPLICATION NUMBER: GB 0100286.4
  PRIOR FILING DATE: 2001-01-05
  NUMBER OF SEQ ID NOS: 1
  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-276-947-1
 Query Match
                     89.7%; Score 1918.5; DB 12; Length 390;
 Best Local Similarity 90.6%; Pred. No. 6.5e-171;
 Matches 365; Conservative 10; Mismatches
                                        15; Indels
                                                    13; Gaps
                                                               1:
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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           Db
         1 MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
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           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
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        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
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           121 YDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNNSWR 180
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        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
           Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
           Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
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RESULT 6
US-09-214-592-33
; Sequence 33, Application US/09214592A
 Publication No. US20030027218A1
: GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEO ID NOS: 34
  SOFTWARE:
; SEQ ID NO 33
   LENGTH: 390
   TYPE: PRT
   ORGANISM: simian
US-09-214-592-33
 Query Match
                     89.6%; Score 1916.5; DB 11; Length 390;
 Best Local Similarity 90.3%; Pred. No. 1e-170;
 Matches 364; Conservative 10; Mismatches
                                        16; Indels
                                                    13; Gaps
                                                               1;
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
           1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Dh
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
           241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
Db
Qу
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
           288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
           348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
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US-09-214-592-17
; Sequence 17, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 17
   LENGTH: 391
   TYPE: PRT
   ORGANISM: human
US-09-214-592-17
 Query Match
                     89.3%; Score 1911; DB 11; Length 391;
 Best Local Similarity 90.3%; Pred. No. 3.3e-170;
 Matches 365; Conservative 10; Mismatches
                                         15; Indels
                                                   14; Gaps
                                                               2:
          1 MAPSGLRLLPLLUPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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            1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Dh
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
           121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
Db
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
           181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Db
Qу
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCF 299
            111111
        241 TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----
Db
                                                 -----ALDTNYCF 287
        300 SSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOH 359
Qу
            288 SSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQH 347
Db
        360 NPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
Qу
           Db
        348 NPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
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RESULT 8

US-09-756-283A-23

; Sequence 23, Application US/09756283A

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; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEO ID NO 23
   LENGTH: 390
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-756-283A-23
 Query Match
                     89.2%; Score 1907.5; DB 10; Length 390;
 Best Local Similarity
                    90.1%; Pred. No. 7e-170;
 Matches 363; Conservative 10; Mismatches 17; Indels
                                                    13; Gaps
                                                               1:
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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           Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHHEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           121 YDKFKQSTHSTYMFFNISELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
           Db
        241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR---
                                                  ----ALDTNYCFS 287
Qу
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
           Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
           Dh
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
US-09-214-592-28
; Sequence 28, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
; APPLICANT: Shibata, CKenji
```

```
APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEO ID NOS: 34
  SOFTWARE:
; SEQ ID NO 28
   LENGTH: 390
   TYPE: PRT
   ORGANISM: canine
US-09-214-592-28
 Query Match
                     88.6%; Score 1895.5; DB 11; Length 390;
 Best Local Similarity 89.6%; Pred. No. 9.3e-169;
 Matches 361; Conservative 12; Mismatches 17; Indels
                                                    13; Gaps
                                                               1:
Qу
         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
           Db
         1 MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLS 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
         61 SPPSOGEVPPVPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKI 120
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
           121 YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRLKLKAEQHVELYQKYSNDSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181 YLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFRLSAHCSCDSKDNTLQVDINGFS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
             111111
        241 SSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 360
Qу
           Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
Qу
           Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 10
US-09-214-592-20
; Sequence 20, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
 APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
; APPLICANT: Sato, CYasufumi
```

```
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEQ ID NOS: 34
  SOFTWARE:
; SEQ ID NO 20
   LENGTH: 390
   TYPE: PRT
   ORGANISM: murine
US-09-214-592-20
 Query Match
                     85.9%; Score 1837.5; DB 11; Length 390;
 Best Local Similarity 85.9%; Pred. No. 2.5e-163;
 Matches 346; Conservative 15; Mismatches
                                         29; Indels
                                                     13; Gaps
                                                                1;
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
           1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
           61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
            Db
        121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
             111111
        241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
           Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            348 PGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 11
US-09-214-592-23
; Sequence 23, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
 APPLICANT: Shibata, CKenji
 APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
```

```
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEO ID NOS: 34
  SOFTWARE:
; SEQ ID NO 23
   LENGTH: 390
   TYPE: PRT
   ORGANISM: rat
US-09-214-592-23
 Query Match
                     85.9%; Score 1837.5; DB 11; Length 390;
 Best Local Similarity 85.9%; Pred. No. 2.5e-163;
 Matches 346; Conservative 14; Mismatches
                                         30; Indels
                                                     13; Gaps
                                                                1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
Qу
            61 SPPSOGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
                  Db
        121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
             111111
        241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
            Db
        348 PGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 12
US-09-214-592-25
; Sequence 25, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
 FILE REFERENCE: 11060
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CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEO ID NOS: 34
  SOFTWARE:
; SEQ ID NO 25
   LENGTH: 315
   TYPE: PRT
   ORGANISM: bovine
US-09-214-592-25
 Query Match
                      73.6%; Score 1574.5; DB 11; Length 315;
 Best Local Similarity 89.9%; Pred. No. 7.4e-139;
 Matches 295; Conservative
                          9; Mismatches
                                           11: Indels
                                                       13; Gaps
                                                                  1;
Qу
         76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
            Db
          1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
        136 NTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
Qу
            Db
         61 NTSELREAVPEPVLLSRADVRLLRLKLKVEOHVELYOKYSNNSWRYLSNRLLAPSDSPEW 120
Qу
        196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
            Db
        121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
        256 PFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDF 315
Qу
            ----ALDTNYCFSSTEKNCCVRQLYIDF 227
Db
        181 PFLLLMATPLERAQHLHSSRHRR----
Qу
        316 RKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALE 375
            Dh
        228 RKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALE 287
        376 PLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            11111111111111111111111111111111111
Db
        288 PLPIVYYVGRKPKVEQLSNMIVRSCKCS 315
RESULT 13
US-09-756-283A-20
; Sequence 20, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
 APPLICANT: Adams, Gillian
 TITLE OF INVENTION: Latent Fusion Protein
 FILE REFERENCE: 0623.1000000
 CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
   LENGTH: 455
   TYPE: PRT
   ORGANISM: Artificial Sequence
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FEATURE:
   OTHER INFORMATION: LAP-mIFN
                            construct
US-09-756-283A-20
 Query Match
                     59.0%; Score 1262.5; DB 10; Length 455;
 Best Local Similarity
                     90.5%; Pred. No. 2e-109;
 Matches 248; Conservative 10; Mismatches 15; Indels
                                                      1; Gaps
                                                                1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            Db
          1 MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qу
         61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
Qу
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
            Db
        121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSW 180
        180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGF 239
Qу
            Db
        181 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGF 240
Qу
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAOHLHS 273
            Db
        241 TTGRRGDLATIHGMNRPFLLLMATPLERAOHLOS 274
RESULT 14
US-09-756-283A-22
; Sequence 22, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
  APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
  FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
 SEO ID NO 22
   LENGTH: 447
   TYPE: PRT
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: mIFN -LAP construct
US-09-756-283A-22
 Query Match
                     53.2%; Score 1139; DB 10; Length 447;
 Best Local Similarity
                     87.0%; Pred. No. 7e-98;
 Matches 228; Conservative 10; Mismatches
                                         18: Indels
                                                         Gaps
                                                                3;
                                                      6:
Qу
         14 PL-LWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGP 72
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Db
        190 PLGLW----AGGGSAAALSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSOGEVPPGP 245
         73 LPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLY 132
Qу
            Db
        246 LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKOSTHSIY 305
        133 MLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSD 191
Qу
            Db
        306 MFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEOHVELYOKYSNNSWRYLSNRLLAPSD 365
        192 SPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIH 251
Qу
            Db
        366 SPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGRRGDLATIH 425
        252 GMNRPFLLLMATPLERAQHLHS 273
Qу
            Db
        426 GMNRPFLLLMATPLERAQHLQS 447
RESULT 15
US-09-214-592-32
; Sequence 32, Application US/09214592A
; Publication No. US20030027218A1
: GENERAL INFORMATION:
  APPLICANT: Yamasaki, CMotoo
  APPLICANT: Shibata, CKenji
  APPLICANT: Sato, CYasufumi
  TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
  TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
  FILE REFERENCE: 11060
  CURRENT APPLICATION NUMBER: US/09/214,592A
  CURRENT FILING DATE: 1999-01-18
  NUMBER OF SEO ID NOS: 34
  SOFTWARE:
; SEQ ID NO 32
   LENGTH: 373
   TYPE: PRT
   ORGANISM: chicken
US-09-214-592-32
 Query Match
                      49.0%; Score 1049; DB 11; Length 373;
 Best Local Similarity 53.5%; Pred. No. 1.4e-89;
 Matches 207; Conservative 52; Mismatches 100; Indels
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                                                      28; Gaps
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
Qу
            Db
          2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
         90 GES-VEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
             : : | |: : :|:|||: |: | : : : :::
                                              Db
         62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
        149 LLSRAELRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
Qу
                              121 LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
Db
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204 VROWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258 Qу 1 | | | | : | : | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | Db 181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239 259 LLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFR 316 Qу Db 240 LAMALPAERANELHSARRRR-------DLDTDYCFGPGTDEKNCCVRPLYIDFR 286 317 KDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEP 376 Qу 287 KDLQWKWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPQTLDP 346 Dh 377 LPIVYYVGRKPKVEQLSNMIVRSCKCS 403 Qу

Search completed: October 28, 2003, 09:28:02 Job time: 25.4507 secs

|||:||||| :|||||:||:||| 347 LPIIYYVGRNVRVEQLSNMVVRACKCS 373

> GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 00:37:16; Search time 13.3169 Seconds

(without alignments)

2910.285 Million cell updates/sec

Title: US-10-017-372E-33

Perfect score: 2139

Db

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		૪				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	2035.5	95.2	390	2	A27512	transforming growt
2	2004	93.7	391	2	S01413	transforming growt
3	1931.5	90.3	390	2	I46463	transforming growt
4	1918.5	89.7	390	1	WFHU2	transforming growt
5	1916.5	89.6	390	2	A26960	transforming growt
6	1895.5	88.6	390	2	JC4023	transforming growt
7	1837.5	85.9	390	1	WFMS2	transforming growt
8	1837.5	85.9	390	2	S10219	transforming growt
9	1574.5	73.6	315	2	A40057	transforming growt
10	1049	49.0	373	2	A41918	transforming growt
11	873.5	40.8	412	2	A34939	transforming growt
12	870.5	40.7	382	2	B61036	transforming growt
13	836	39.1	409	2	S01825	transforming growt
14	832.5	38.9	410	2	A41397	transforming growt
15	831.5	38.9	410	2	A55706	transforming growt
16	829.5	38.8	412	2	A36169	transforming growt
17	829	38.8	414	1	WFMSB2	transforming growt
18	814	38.1	414	1	WFMKB2	transforming growt
19	814	38.1	414	2	A31249	transforming growt
20	813.5	38.0	413	1	WFXLB2	transforming growt
21	813	38.0	412	2	A39489	transforming growt
22	798	37.3	442	2	B31249	transforming growt
23	693.5	32.4	130	2	I48196	transforming growt
24	482	22.5	112	2	A61439	transforming growt
25	279	13.0	425	2	I47072	inhibin beta-A cha
26	276.5	12.9	424	1	WFPGBA	inhibin beta-A cha
27	274.5	12.8	424	1	S31440	inhibin beta-A cha
28	274	12.8	425		S50898	inhibin beta-A cha
29	272.5	12.7	426	1	B24248	inhibin beta-A cha
30	270.5	12.6	424	1	B40905	inhibin beta-A cha
31	260.5	12.2	398	2	JH0688	bone morphogenetic
32	259	12.1	398	2	JH0687	bone morphogenetic
33	257.5	12.0	413	2	JC4862	activin beta-A cha
34	257.5	12.0	394		S45355	bone morphogenetic
35	255	11.9	396		BMHU2	bone morphogenetic
36	253.5	11.9	513	1	BMHU6	bone morphogenetic
37	247.5	11.6	393	2	S37073	bone morphogenetic
38	247.3	11.5	510	2	A54798	Vg-1-related prote
38		11.5				activin beta E cha
	240		350		JC5241	TGF-beta-related p
40	237	11.1	455	2	A43918	-
41	233.5	10.9	402	2	A45056	osteogenic protein
42	233	10.9	420		149541	bone morphogenetic
43	232	10.8	454		BMHU5	bone morphogenetic
44	229.5	10.7	461	2	S52408	SPDVR1 protein - s
45	227	10.6	367	2	JC4151	activin beta D cha

```
transforming growth factor beta-1 precursor - pig
N; Alternate names: TGF-beta
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Jun-1988 #sequence revision 05-Jun-1988 #text_change 16-Jul-1999
C; Accession: A27512; A26356; I46657
R; Derynck, R.; Rhee, L.
Nucleic Acids Res. 15, 3187, 1987
A; Title: Sequence of the porcine transforming growth factor-beta precursor.
A; Reference number: A27512; MUID: 87174844; PMID: 3470708
A; Accession: A27512
A; Molecule type: mRNA
A; Residues: 1-390 < DER>
R; Cheifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.;
Lucas, R.; Massague, J.
Cell 48, 409-415, 1987
A; Title: The transforming growth factor-beta system, a complex pattern of cross-
reactive ligands and receptors.
A; Reference number: A90890; MUID: 87102890; PMID: 2879635
A; Accession: A26356
A; Molecule type: protein
A; Residues: 279-322 < CHE>
R; Kondaiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn,
M.B.; Roberts, A.B.
J. Biol. Chem. 263, 18313-18317, 1988
A; Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
Evidence for alternate splicing and polyadenylation.
A; Reference number: I46657; MUID: 89054010; PMID: 2461367
A; Accession: I46657
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-390 < KON>
A; Cross-references: GB: M23703; NID: q755044; PIDN: AAA64616.1; PID: q755045
C;Genetics:
A;Gene: TGFB; TGF-beta-1
C; Superfamily: inhibin
C; Keywords: growth factor
                        95.2%; Score 2035.5; DB 2; Length 390;
 Query Match
                        96.0%; Pred. No. 1.2e-155;
 Best Local Similarity
 Matches 387; Conservative 0; Mismatches
                                               3; Indels
                                                           13;
                                                               Gaps
                                                                       1;
           1 MAPSGLRLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
             1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
          61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
             Db
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
             Db
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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             Db
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
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A27512

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241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
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           241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
           288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Dh
RESULT 2
S01413
transforming growth factor beta-1 precursor - chicken
C; Species: Gallus gallus (chicken)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C; Accession: S01413
R; Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A; Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-
beta 1).
A; Reference number: S01413; MUID: 88335639; PMID: 3166520
A; Accession: S01413
A; Molecule type: DNA
A; Residues: 1-391 < JAK>
A; Cross-references: EMBL: X12373; NID: g63808; PIDN: CAA30933.1; PID: g63809
C; Superfamily: inhibin
C; Keywords: growth factor
 Query Match
                     93.7%; Score 2004; DB 2; Length 391;
 Best Local Similarity
                     95.0%; Pred. No. 4e-153;
 Matches 384; Conservative
                                          6; Indels
                           0; Mismatches
                                                     14; Gaps
                                                                2;
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          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            1 MPPSGPGLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
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            61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
Qу
            121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWG 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEIN-GF 239
Qу
            181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINAGF 240
Db
        240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCF 299
Qу
            111111
Dh
        241 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR------ALDTNYCF 287
        300 SSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQH 359
Qу
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Db
        288 SSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQH 347
        360 NPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
           348 NPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391
Db
RESULT 3
I46463
transforming growth factor beta-1 - sheep
C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C; Date: 19-Dec-1997 #sequence revision 19-Dec-1997 #text change 24-Nov-1999
C; Accession: I46463; S45115
R; Woodall, C.J.; McLaren, L.J.; Watt, N.J.
Gene 150, 371-373, 1994
A; Title: Sequence and chromosomal localisation of the gene encoding ovine latent
transforming growth factor-beta 1.
A; Reference number: I46463; MUID: 95121932; PMID: 7821809
A; Accession: I46463
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-390 < WOO>
A; Cross-references: EMBL: X76916; NID: g496648; PIDN: CAA54242.1; PID: g496649
A; Note: submitted to the EMBL Data Library, December 1993
C; Superfamily: inhibin
 Query Match
                     90.3%; Score 1931.5; DB 2; Length 390;
 Best Local Similarity 90.6%; Pred. No. 2.6e-147;
 Matches 365; Conservative 10; Mismatches
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         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Qy
           1 MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKGIEAIRGQILSKLRLA 60
Db
        61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
           Db
        61 SPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
           121 YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEOHVELYOKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
           181\ \mathtt{YLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREE1EGFRLSAHCSCDSKDNTLQVDINGFS}\ 240
Db
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
           241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHN 360
Qу
           288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
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RESULT 4
WFHU2
transforming growth factor beta-1 precursor [validated] - human
N; Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C; Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text change 08-Dec-2000
C; Accession: A27513; A01395; A22290; I59664; S53444
R; Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A; Title: Intron-exon structure of the human transforming growth factor-beta
precursor gene.
A; Reference number: A27513; MUID: 87174845; PMID: 3470709
A; Accession: A27513
A; Molecule type: DNA
A; Residues: 1-390 < DER>
A; Cross-references: GB: X05839; GB: Y00112; NID: q37097; PIDN: CAA29283.1;
PID:q1212989
R; Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian,
R.K.; Roberts, A.B.; Sporn, M.B.; Goeddel, D.V.
Nature 316, 701-705, 1985
A; Title: Human transforming growth factor-beta complementary DNA sequence and
expression in normal and transformed cells.
A; Reference number: A01395; MUID: 85296301; PMID: 3861940
A; Accession: A01395
A; Molecule type: mRNA
A; Residues: 1-9, 'P', 11-24, 'P', 26-159, 'R', 160-390 < DE2>
A;Cross-references: GB:X02812; GB:J05114; NID:g37092; PIDN:CAA26580.1;
PID: g37093
A; Note: the authors suggest that residues 8-23 could represent the hydrophobic
core of an amino-terminal signal peptide
R; Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A; Title: Cellular receptors for type beta transforming growth factor. Ligand
binding and affinity labeling in human and rodent cell lines.
A; Reference number: A22290; MUID: 85131019; PMID: 2982829
A; Accession: A22290
A; Molecule type: protein
A; Residues: 279-295, 'XX', 298-301 < MAS>
R; Urushizaki, Y.; Niitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.;
Urushizaki, I.; Takahashi, Y.; Ito, H.
Tumor Res. 22, 41-55, 1987
A; Title: Cloning and expression of the gene for human transforming growth
factor-beta in Escherichia coli.
A; Reference number: 159664
A; Accession: I59664
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 279-390 < RES>
A; Cross-references: GB: M38449; NID: g339557; PIDN: AAA36735.1; PID: g339558
R; Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.;
Marshak, D.R.; Haley, J.D.
Biochem. J. 305, 87-92, 1995
A; Title: Physical and biological characterization of a growth-inhibitory
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activity purified from the neuroepithelioma cell line A673.

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A; Reference number: S53444; MUID: 95126934; PMID: 7826358
A; Accession: S53444
A; Status: preliminary
A; Molecule type: protein
A; Residues: 279-297 <STA>
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor
polypeptide; the active molecule is a dimer of identical polypeptide chains
linked by an interchain disulfide bond.
C:Genetics:
A; Gene: GDB: TGFB1; TGFB
A; Cross-references: GDB:120729; OMIM:190180
A; Map position: 19g13.2-19g13.2
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 89.7%; Score 1918.5; DB 1; Length 390; Best Local Similarity 90.6%; Pred. No. 2.9e-146;
 Matches 365; Conservative 10; Mismatches
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          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120
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         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
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            241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTNYCFS 287
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        301 STEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 360
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        361 PGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
            Db
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C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text change 24-Nov-1999
C; Accession: A26960
R; Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987
A; Title: Cloning and sequence analysis of simian transforming growth factor-beta
CDNA.
A; Reference number: A26960; MUID: 87246074; PMID: 3474130
A; Accession: A26960
A; Molecule type: mRNA
A; Residues: 1-390 < SHA>
A; Cross-references: GB: M16658; NID: q176552; PIDN: AAA35369.1; PID: q176553
C; Superfamily: inhibin
C; Keywords: growth factor
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-390/Product: transforming growth factor beta #status predicted <MAT>
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                      89.6%; Score 1916.5; DB 2; Length 390;
 Best Local Similarity 90.3%; Pred. No. 4.2e-146;
 Matches 364; Conservative 10; Mismatches
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Db
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
            61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
            121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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Db
Qу
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
            241 TGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRHRR-----ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 347
Db
Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
            Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 6
JC4023
transforming growth factor beta-1 - dog
C; Species: Canis lupus familiaris (dog)
C;Date: 13-Jun-1995 #sequence revision 14-Jul-1995 #text change 24-Nov-1999
C; Accession: JC4023
R; Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
Gene 155, 307-308, 1995
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A; Title: Cloning of a canine cDNA homologous to the human transforming growth
factor-beta 1-encoding gene.
A; Reference number: JC4023; MUID: 95237630; PMID: 7721110
A; Accession: JC4023
A; Molecule type: mRNA
A; Residues: 1-390 <MAN>
A; Cross-references: GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072
C; Comment: This factor plays a multifunctional role as a regulator of mammalian
cell growth and as a modulator of immune responses.
C; Genetics:
A; Gene: tgf-beta1
C; Superfamily: inhibin
C; Keywords: growth factor; transforming protein
F;288-390/Product: transforming growth factor beta 1 #status predicted <MAT>
                      88.6%; Score 1895.5; DB 2; Length 390;
 Best Local Similarity 89.6%; Pred. No. 2e-144;
 Matches 361; Conservative 12; Mismatches 17; Indels
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                                                                 1:
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          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
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            Db
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        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
            241 SSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQRR------ALDTNYCFS 287
Db
Qу
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Db
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Qу
            Db
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RESULT 7
WFMS2
transforming growth factor beta-1 precursor - mouse
N; Alternate names: TGF type 2; TGF-beta
C; Species: Mus musculus (house mouse)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 24-Nov-1999
C; Accession: A01396
R; Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
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A; Title: The murine transforming growth factor-beta precursor.
A; Reference number: A01396; MUID: 86168129; PMID: 3007454
A; Accession: A01396
A; Molecule type: mRNA
A; Residues: 1-390 < DER>
A;Cross-references: GB:M13177; NID:g201952; PIDN:AAA40423.1; PID:g201953
A; Note: the authors suggest that residues 8-23 could represent the hydrophobic
core of an amino-terminal signal peptide
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor
polypeptide; the active molecule is a dimer of identical polypeptide chains
linked by an interchain disulfide bond.
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen;
transformation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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 Matches 346; Conservative 15; Mismatches
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Qу
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Qу
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            Db
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        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
            121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180
Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240
Db
Qy
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
              241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR------ALDTNYCFS 287
Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            Db
        348 PGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
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C; Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text change 24-Nov-1999
C; Accession: S10219; PT0023; S02267
R; Qian, S.W.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
Nucleic Acids Res. 18, 3059, 1990
A; Title: cDNA cloning by PCR of rat transforming growth factor beta-1.
A; Reference number: S10219; MUID: 90272425; PMID: 2349108
A; Accession: S10219
A; Molecule type: mRNA
A; Residues: 1-390 < QIA>
A;Cross-references: EMBL:X52498; NID:g57341; PIDN:CAA36741.1; PID:g57342
R;Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
J. Biochem. 106, 304-310, 1989
A; Title: Purification and structural analysis of a latent form of transforming
growth factor-beta from rat platelets.
A; Reference number: PT0023; MUID: 90036779; PMID: 2478527
A: Accession: PT0023
A; Molecule type: protein
A; Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 < OKA>
R; Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
FEBS Lett. 242, 240-244, 1989
A; Title: One of two subunits of masking protein in latent TGF-beta is a part of
pro-TGF-beta.
A; Reference number: S02267; MUID: 89121078; PMID: 2914605
A; Accession: S02267
A; Molecule type: protein
A; Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 < OK2>
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; integrin binding
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-278/Domain: propeptide #status experimental <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match
                       85.9%; Score 1837.5; DB 2; Length 390;
 Best Local Similarity 85.9%; Pred. No. 9.2e-140;
 Matches 346; Conservative 14; Mismatches
                                             30; Indels
                                                          13; Gaps
                                                                      1;
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
QУ
             1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
             61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
Dh
Qу
         121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
                    Db
         121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
         181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
             181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
Db
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
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Db
          241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR------ALDTNYCFS 287
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          301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
              288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
Qу
          361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
              Db
          348 PGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
A40057
transforming growth factor beta-1 precursor - bovine (fragment)
N; Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or
dEGF; MGF-b; milk growth factor b; TGF-type II
C; Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C; Accession: A40057; A42320; A05284; A24322; B61439
R; Van Obberghen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker,
C.C.
Mol. Endocrinol. 1, 693-698, 1987
A; Title: Complementary deoxyribonucleic acid cloning of bovine transforming
growth factor-betal.
A; Reference number: A40057; MUID: 91042552; PMID: 3153459
A; Accession: A40057
A; Molecule type: mRNA
A; Residues: 1-315 < VAN>
A; Cross-references: GB: M36271; NID: g163747; PIDN: AAA30778.1; PID: g163748
R; Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A; Title: Purification and characterization of transforming growth factor-beta2.3
and -betal.2 heterodimers from bovine bone.
A; Reference number: A42320; MUID: 92129307; PMID: 1733936
A; Accession: A42320
A; Molecule type: protein
A; Residues: 204-209, 'X', 211-217 < OGA>
R; Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan,
Y.C.E.; Stein, S.; Lehrman, S.R.; Smith, J.M.; Lamb, L.C.; Sporn, M.B.
Biochemistry 22, 5692-5698, 1983
A; Title: Purification and properties of a type beta transforming growth factor
from bovine kidney.
A; Reference number: A05284; MUID: 84104793; PMID: 6607069
A; Accession: A05284
A; Molecule type: protein
A; Residues: 204-218 < ROB>
R; Seyedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti,
A.; Siegel, N.R.; Galluppi, G.R.; Piez, K.A.
J. Biol. Chem. 261, 5693-5695, 1986
A; Title: Cartilage-inducing factor-A. Apparent identity to transforming growth
factor-beta.
A; Reference number: A24322; MUID: 86195954; PMID: 3754555
A; Accession: A24322
A; Molecule type: protein
A; Residues: 204-233 <SEY>
R;Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
```

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A; Title: Separation, purification, and sequence identification of TGF-betal and
TGF-beta2 from bovine milk.
A; Reference number: A61439; MUID: 92189724; PMID: 1799413
A; Accession: B61439
A; Molecule type: protein
A; Residues: 204-209, 'X', 211-217, 'XX', 220-232 <JIN>
C; Comment: This polypeptide is composed of two polypeptide chains cross-linked
by disulfide bonds. It has been found in neoplastic and non-neoplastic tissues.
C; Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic
mitogenic activity, but in soft agar, it reacts synergistically with either type
I TFG or EGF, and induces cell proliferation. Cells grown in monolayer do not
respond in a similar manner to these growth factors, but morphologically do
acquire a transformed phenotype.
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; heterodimer
F;204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F;7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
                       73.6%; Score 1574.5; DB 2; Length 315;
  Query Match
                       89.9%; Pred. No. 9e-119;
 Best Local Similarity
 Matches 295; Conservative
                             9: Mismatches
                                            11: Indels
                                                         13: Gaps
                                                                     1:
          76 AVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
Qу
            Db
           1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
         136 NTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
Qу
             61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
Db
         196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
Qу
            121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
Db
         256 PFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDF 315
Qу
             1111111111
                                            181 PFLLLMATPLERAOHLHSSRHRR-----ALDTNYCFSSTEKNCCVROLYIDF 227
Dh
         316 RKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASAAPCCVPOALE 375
QУ
            Db
         228 RKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASAAPCCVPOALE 287
         376 PLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
Qу
             288 PLPIVYYVGRKPKVEOLSNMIVRSCKCS 315
Db
RESULT 10
A41918
transforming growth factor beta-4 precursor - chicken (fragment)
N; Alternate names: TGF-beta 4
C; Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C; Accession: A41918; A34941; S03110
R; Burt, D.W.; Jakowlew, S.B.
Mol. Endocrinol. 6, 989-992, 1992
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A; Title: Correction: a new interpretation of a chicken transforming growth
factor-beta 4 complementary DNA.
A; Reference number: A41918; MUID: 92357039; PMID: 1353860
A; Accession: A41918
A; Molecule type: mRNA
A; Residues: 1-373 <BUR>
A; Cross-references: GB: M31160; GB: X08012; GB: S41706; NID: g1262437;
PIDN:AAB05637.1; PID:g1262438
A; Note: sequence extracted from NCBI backbone (NCBIN:110186, NCBIP:110187)
A; Note: this report corrects and reinterprets the sequence from reference A34941
R; Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 1186-1195, 1988
A; Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic
acid encoding transforming growth factor beta-4 from chicken embryo
chondrocytes.
A; Reference number: A34941; MUID: 89112198; PMID: 2464131
A:Accession: A34941
A; Molecule type: mRNA
A; Residues: 'MDPMSIGPKSCGGSPWRPPGTAPWSIGSRRATASSSCSTSSRVRAEVGGRAL', 122-
209, 'D', 211-373 <JAK>
A; Cross-references: EMBL: X08012
A; Note: this sequence has been corrected in A41918
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor
F;1/Domain: signal sequence (fragment) #status predicted <SIG>
F;223-225/Region: cell attachment (R-G-D) motif
F;260-373/Product: transforming growth factor beta-4 #status predicted <MAT>
F;54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted
                       49.0%; Score 1049; DB 2; Length 373;
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 Best Local Similarity 53.5%; Pred. No. 1.8e-76;
 Matches 207; Conservative 52; Mismatches 100; Indels
                                                        28; Gaps
                                                                    8;
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
Qу
            2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
Db
         90 GES-VEPEPEADYYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
              62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
Db
Qу
        149 LLSRAELRLKLK-----VEOHVELYOKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
                              121 LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
Db
        204 VROWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
Qу
            181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEO-QRGDMOSIAKKHRRVPYV 239
Db
Qу
        259 LLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCF--SSTEKNCCVRQLYIDFR 316
                                                 Db
        240 LAMALPAERANELHSARRRR------DLDTDYCFGPGTDEKNCCVRPLYIDFR 286
        317 KDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEP 376
Qу
            287 KDLQWKWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPQTLDP 346
Db
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Qу
          377 LPIVYYVGRKPKVEQLSNMIVRSCKCS 403
              111:1111 : 11111 : 11:111
Db
          347 LPIIYYVGRNVRVEQLSNMVVRACKCS 373
RESULT 11
A34939
transforming growth factor beta-3 precursor - chicken
C; Species: Gallus gallus (chicken)
C;Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 16-Jul-1999
C; Accession: A34939; S25850; S36125; S36124; I51181
R; Jakowlew, S.B.; Dillard, P.J.; Kondaiah, P.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 747-755, 1988
A; Title: Complementary deoxyribonucleic acid cloning of a novel transforming
growth factor-beta messenger ribonucleic acid from chick embryo chondrocytes.
A; Reference number: A34939; MUID: 89096966; PMID: 3211158
A; Accession: A34939
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-412 < JAK>
A; Cross-references: GB: M31154; NID: q212758; PIDN: AAA49089.1; PID: q212759
R; Burt, D.W.; Paton, I.R.; Dey, B.R.
J. Mol. Endocrinol. 7, 175-183, 1991
A; Title: Comparative analysis of human and chicken transforming growth factor-
beta-2 and -beta-3 promoters.
A; Reference number: S25850; MUID: 92134496; PMID: 1840616
A; Accession: S25850
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-117 <BUR>
A; Cross-references: EMBL: X58127; NID: q63815; PIDN: CAA41128.1; PID: q63816
A; Accession: S36125
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 119-172 < BU2>
A; Cross-references: EMBL: X60055; NID: g396688; PIDN: CAA42653.1; PID: g396689
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
A; Accession: S36124
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A; Residues: 173-322, 'ELPT', 327-412 <BU3>
A; Cross-references: EMBL: X60091
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
1991
R; Jakowlew, S.B.; Lechleider, R.; Geiser, A.G.; Kim, S.J.; Santa-Coloma, T.A.;
Cubert, J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 6, 1285-1298, 1992
A; Title: Identification and characterization of the chicken transforming growth
factor-beta 3 promoter.
A; Reference number: I51181; MUID: 93024487; PMID: 1406706
A; Accession: I51181
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-117 < JA2>
A;Cross-references: GB:S46000; NID:g257172; PIDN:AAB23575.1; PID:g257173
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C; Genetics:

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A; Introns: 216/1; 252/1; 309/2; 360/3
A; Note: list of introns may be incomplete
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-3 #status predicted <MAT>
F;74,142/Binding site: carbohydrate (Asn) (covalent) #status predicted
                      40.8%; Score 873.5; DB 2; Length 412;
 Query Match
 Best Local Similarity 46.6%; Pred. No. 2.5e-62;
 Matches 198; Conservative 56; Mismatches 114; Indels 57; Gaps
                                                                  14;
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
Qу
            Db
          9 LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP 66
         75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNQIYDKF 124
Qу
              | | : :
         67 YOILALYNSTRELL--EEMEEEKEESCSOENTESEYYAKEIHKFDMIOGLPEHNELGICP 124
Db
        125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEOHVELYOKYSND--- 177
Qу
               1 111 1:11:
                                                125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEORIELFOILRPDEHI 180
Db
        178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
Qу
               Db
        181 AKQRYLSGRNVQTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE 240
        230 N---TLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAQH--LHSSRHRR 278
Qу
                | :: | :|
                             Db
        241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR 300
        279 ALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 338
Qу
                       Db
                  -----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYFANFCSGP 347
        339 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 398
Qу
            Db
        348 CPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 407
        399 SCKCS 403
Qу
            Db
        408 SCKCS 412
RESULT 12
B61036
transforming growth factor beta-5 precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text change 16-Jul-1999
C; Accession: A34929; B61036
R; Kondaiah, P.; Sands, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn,
M.B.; Melton, D.A.
J. Biol. Chem. 265, 1089-1093, 1990
A; Title: Identification of a novel transforming growth factor-beta (TGF-beta5)
mRNA in Xenopus laevis.
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A; Reference number: A34929; MUID: 90110090; PMID: 2295601
A; Accession: A34929
A; Molecule type: mRNA
A; Residues: 1-382 < KON>
A; Cross-references: GB: J05180; NID: q214821; PIDN: AAA49968.1; PID: q214822
R; Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert,
M.L.; Kondaiah, P.; Danielpour, D.; Kehrl, J.H.; Wahl, S.M.; Dawid, I.B.; Sporn,
M.B.
Growth Factors 2, 135-147, 1990
A; Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium
conditioned by Xenopus XTC cells.
A; Reference number: A61036; MUID: 90253806; PMID: 2340184
A; Accession: B61036
A; Molecule type: protein
A; Residues: 271-276, 'X', 278-284, 'XX', 287-299 < ROB>
C; Superfamily: inhibin
C; Keywords: growth factor
F;271-382/Product: transforming growth factor beta-5 #status experimental <MAT>
 Query Match
                       40.7%; Score 870.5; DB 2; Length 382;
 Best Local Similarity 46.3%; Pred. No. 4e-62;
 Matches 190; Conservative 55; Mismatches 122; Indels 43; Gaps
                                                                   11:
Qу
          9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
            1 MEVLWMLLVLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGOILSKLKLDKTPDV-DS 59
Db
         69 PPGPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDK 123
Qу
                : [[[]]:]
                                                         - | | | | | | | |
         60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED- 115
Db
Qу
         124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEOHVELYOKYSNDSW-- 179
                      Db
         116 ----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKQTDKNMDQRMELFWKYQENGTTH 170
         180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
Qу
             | | | | :: : |
                         : :||
         171 SRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEQFGLQPACKCPTPQAKD----ID 226
Db
         236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKAL 293
Qу
                   1 11
         227 IEGF-PALRGDLASLSSKENTKPYLMITSMPAERIDTVTSSRKKR------GV 272
Db
         294 DTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVL 353
Qу
               Db
         273 GQEYCFGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQYSKVL 332
Qу
         354 ALYNOHNPGASAAPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
            Db
         333 SLYNQNNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVVRSCNCS 382
RESULT 13
S01825
transforming growth factor beta-3 precursor - pig
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1989 #sequence revision 30-Sep-1989 #text change 16-Jul-1999
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C; Accession: S01825
R; Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee,
L.; Mason, A.J.; Miller, D.A.; Coffey, R.J.; Moses, H.L.; Chen, E.Y.
EMBO J. 7, 3737-3743, 1988
A; Title: A new type of transforming growth factor-beta, TGF-beta3.
A; Reference number: S01824; MUID: 89091120; PMID: 3208746
A; Accession: S01825
A; Molecule type: mRNA
A; Residues: 1-409 < DER>
A; Cross-references: EMBL: X14150; NID: q2127; PIDN: CAA32363.1; PID: q2128
C; Superfamily: inhibin
C; Keywords: growth factor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-297/Domain: propeptide #status predicted <PRO>
F;298-409/Product: transforming growth factor beta-3 #status predicted <MAT>
 Query Match
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 Best Local Similarity 45.0%; Pred. No. 2.6e-59;
 Matches 190; Conservative 58; Mismatches 122; Indels 52; Gaps
                                                                  14;
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
Qу
                     Db
          7 LVVLALLNFATVSLSMSTCTTLDFDHIKRKRVEAIRGOILSKLRLTSPPDPSML--ANIP 64
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNQIYDKFKG 126
QУ
                       65 TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124
Db
Qу
        127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
               :: || | : :
                                | ||| |:||:
                                              : || :||:|
        125 ITSKIFR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180
Db
Qу
        179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
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Db
        181 QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240
Qу
        231 --TLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAOH--LHSSRHRRALD 281
              : :: | :|
                           Db
        241 QEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLILMMIPPDRLDNPGLGAQRKKR--- 297
Qу
        282 TNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPY 341
                     Db
        298 -----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPY 347
Qу
        342 IWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCK 401
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        408 CS 409
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C;Date: 03-Apr-1992 #sequence revision 03-Apr-1992 #text change 16-Jul-1999
C; Accession: A41397; A61039; A61225
R; Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R.
Mol. Endocrinol. 3, 1926-1934, 1989
A; Title: Complementary DNA cloning of the murine transforming growth factor-
beta3 (TGFbeta3) precursor and the comparative expression of TGFbeta3 and
TGFbetal messenger RNA in murine embryos and adult tissues.
A; Reference number: A41397; MUID: 90190650; PMID: 2628730
A; Accession: A41397
A; Molecule type: mRNA
A; Residues: 1-410 <MIL>
A; Cross-references: GB: M32745; NID: g201949; PIDN: AAA40422.1; PID: g201950
R; Denhez, F.; Lafyatis, R.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
Growth Factors 3, 139-146, 1990
A; Title: Cloning by polymerase chain reaction of a new mouse TGF-beta, mTGF-
beta3.
A; Reference number: A61039; MUID: 91000714; PMID: 2206556
A; Accession: A61039
A; Molecule type: mRNA
A; Residues: 1-410 < DEN>
R; Watrin, F.; Scotto, L.; Assoian, R.K.; Wolgemuth, D.J.
Cell Growth Differ. 2, 77-83, 1991
A; Title: Cell lineage specificity of expression of the murine transforming
growth factor beta-3 and transforming growth factor beta-1 genes.
A; Reference number: A61225; MUID: 91299576; PMID: 2069871
A; Accession: A61225
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 285-410 <WAT>
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation
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F;259-261/Region: cell attachment (R-G-D) motif
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Db
           7 LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP 64
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Db
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         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
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Db
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Db
         241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRK---- 296
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C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text change 16-Jul-1999
C; Accession: A55706; B40699; \overline{S}36042
R; Wang, J.; Kuliszewski, M.; Yee, W.; Sedlackova, L.; Xu, J.; Tseu, I.; Post, M.
J. Biol. Chem. 270, 2722-2728, 1995
A; Title: Cloning and expression of glucocorticoid-induced genes in fetal rat
lung fibroblasts. Transforming growth factor-beta-3.
A; Reference number: A55706; MUID: 95155340; PMID: 7852342
A; Accession: A55706
A; Molecule type: mRNA
A; Residues: 1-410 <WAN>
A; Cross-references: GB:U03491
A; Note: it is uncertain whether Met-1 is the initiator
R; McKinnon, R.D.; Piras, G.; Ida Jr., J.A.; Dubois-Dalcq, M.
J. Cell Biol. 121, 1397-1407, 1993
A; Title: A role for TGF-beta in oligodendrocyte differentiation.
A; Reference number: A40699; MUID: 93286190; PMID: 8509457
A; Accession: B40699
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 157-211 <MCK>
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C; Superfamily: inhibin
 Query Match
                        38.9%; Score 831.5; DB 2; Length 410;
 Best Local Similarity 44.7%; Pred. No. 5.9e-59;
 Matches 188; Conservative 58; Mismatches 126; Indels
                                                           49; Gaps
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          75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG 126
Qу
               1::
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Db
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Qу
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Qy	231	TLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDT 282
Db	241	: :: :: : : : : : : : :
Qy	283	NDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYI 342
Db	297	: : : : : : :
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Db	350	:
Qy	403	S 403
Db	410	S 410

Search completed: October 28, 2003, 09:09:49 Job time: 14.3169 secs

> GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 00:08:41; Search time 8.07747 Seconds

(without alignments)

2346.251 Million cell updates/sec

Title: US-10-017-372E-33

Perfect score: 2139

Sequence: 1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		٥.			SUMMARIES	1
Dagula		%				
Result	0	Query	7 la	D D	7.0	Description
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1	2032.5				TGF1_PIG	P07200 sus scrofa
2	1931.5		390	1	TGF1_SHEEP	
	1918.5	89.7	390	1	TGF1_HUMAN	P01137 homo sapien
4	1916.5	89.6	390 390 390	1	TGF1_CERAE	P09533 cercopithec
5				1	TGF1_CANFA	P54831 canis famil
6	1841.5		390	1	TGF1_HORSE	Ol9011 equus cabal
7	1837.5		390	1	TGF1_MOUSE	P04202 mus musculu
8	1837.5		390	1	TGF1_RAT	P17246 rattus norv
9	1828.5	85.5	390	1	TGF1_CAVPO	Q9z1y6 cavia porce
10	1574.5	73.6	315	1	TGF1_BOVIN	P18341 bos taurus
11	1049	49.0	373	1	TGF1_CHICK	P09531 gallus gall
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13	854.5	39.9	412	1	TGF3_CHICK	P16047 gallus gall
14	836	39.1	409	1	TGF3_PIG	P15203 sus scrofa
15	832.5	38.9	410	1	TGF3_MOUSE	P17125 mus musculu
16	831.5	38.9	412	1	TGF3_RAT	Q07258 rattus norv
17	829.5	38.8	412	1	TGF3_HUMAN	P10600 homo sapien
18	829	38.8	414	1	TGF2_MOUSE	P27090 mus musculu
19	814	38.1	414	1	TGF2_HUMAN	P08112 homo sapien
20	813.5	38.0	413	1	TGF2_XENLA	P17247 xenopus lae
21	813	38.0	412	1	TGF2_CHICK	P30371 gallus gall
22	810	37.9	435	1	TGF2_PIG	P09858 sus scrofa
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27	315.5	14.7	375	1	GDF8_PIG	018831 sus scrofa
28	314.5	14.7	375	1	GDF8_PAPHA	Ol8828 papio hamad
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31	310.5	14.5	376	1	GDF8_MOUSE	008689 mus musculu
32	309.5	14.5	375	1	GDF8_SHEEP	O18830 ovis aries
33	304	14.2	405	1	GDFB_MOUSE	Q9z1w4 mus musculu
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35	300.5	14.0	375	1	GDF8_BOVIN	Ol8836 bos taurus
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38	279	13.0	425	1	IHBA SHEEP	P43032 ovis aries
39	276.5	12.9	424	1	IHBA_PIG	P03970 sus scrofa
40	274.5	12.8	424	1	IHBA_MOUSE	Q04998 mus musculu
41	274.5	12.8	424	1	IHBA_RAT	P18331 rattus norv
42	274	12.8	425	1	IHBA_BOVIN	P07995 bos taurus
43	273.5	12.8	426	1	IHBA_HORSE	P55102 equus cabal
44	272.5	12.7	426	1	IHBA_HUMAN	P08476 homo sapien
45	269.5	12.6	424	1	IHBA_CHICK	P27092 gallus gall
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RESULT 1
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                                    PRT;
                                           390 AA.
AC
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DT
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DT
     01-APR-1988 (Rel. 07, Last sequence update)
DT
     28-FEB-2003 (Rel. 41, Last annotation update)
DE
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GN
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OS
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OC
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OC
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RX
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RA
     Derynck R., Rhee L.;
RT
     "Sequence of the porcine transforming growth factor-beta precursor.";
RL
     Nucleic Acids Res. 15:3187-3187(1987).
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RX
RA
     Kondaiah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
RA
     Sporn M.B., Roberts A.B.;
     "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
RT
RT
     Evidence for alternate splicing and polyadenylation.";
RL
     J. Biol. Chem. 263:18313-18317(1988).
RN
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RР
     SEQUENCE FROM N.A., AND VARIANT VAL-114.
RX
     MEDLINE=88335639; PubMed=3166520;
RA
     Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT
     "Nucleotide sequence of chicken transforming growth factor-beta 1
     (TGF-beta 1).";
RT
     Nucleic Acids Res. 16:8730-8730(1988).
RL
RN
     [4]
RP
     SHOWS THAT REF.3 SEQUENCE IS FROM PIG.
RA
     Jakowlew S.B.;
RL
     Unpublished observations (MAR-1996).
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     SEQUENCE FROM N.A., AND VARIANT VAL-114.
     Wimmers K., Chomdej S., Ponsuksili S., Schellander K.;
RA
RT
     "Polymorphism in the porcine transforming growth factor beta 1
RT
     gene.";
RL
     Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN
RP
     SEQUENCE OF 279-322.
RX
     MEDLINE=87102890; PubMed=2879635;
RA
     Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
RA
     Lucas R., Massague J.;
RT
     "The transforming growth factor-beta system, a complex pattern of
     cross-reactive ligands and receptors.";
RT
RI.
     Cell 48:409-415(1987).
     -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
```

```
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
     -!- SUBUNIT: Homodimer; disulfide-linked.
CC
     -!- SUBCELLULAR LOCATION: Secreted.
CC
     -!- SIMILARITY: Belongs to the TGF-beta family.
CC
     -!- CAUTION: REF.3 SEQUENCE WHICH WAS SAID TO ORIGINATE FROM CHICKEN
CC
        WHITE LEGHORN, SEEMS (REF.4) TO ORIGINATE FROM PIG.
CC
     CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
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     or send an email to license@isb-sib.ch).
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     _____
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DR
    EMBL; M23703; AAA64616.1; -.
DR
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    EMBL; X12373; CAA30933.1; -.
DR
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    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
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    ProDom; PD000357; TGFb; 1.
DR
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DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
    Growth factor; Mitogen; Glycoprotein; Signal; Polymorphism.
KW
FT
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                       23
              1
                               POTENTIAL.
FT
    PROPEP
                      278
                24
FT
    CHAIN
                279
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                              BY SIMILARITY.
FT
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    DISULFID
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              322
FT
    DISULFID
                      387
                              BY SIMILARITY.
FT
    DISULFID
             326
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FT
    DISULFID
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FT
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FT
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                      246
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FT
                     114
    VARIANT
                               L -> V.
FT
    CONFLICT
                6
                       7
                               LR -> PG (IN REF. 3).
FT
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                     180
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                     237
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 Query Match 95.0%; Score 2032.5; DB 1; Length 390; Best Local Similarity 95.8%; Pred. No. 1.9e-152;
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                                           3; Indels
                                                     13; Gaps
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Qу
            1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
Db
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Qу
            61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMLESGNOI 120
Db
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Qу
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Dh
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Qу
            181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
            11111111
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----
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                                                  ----ALDTNYCFS 287
        301 STEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHN 360
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            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
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        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 2
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                             PRT:
                                   390 AA.
AC
    P50414;
    01-OCT-1996 (Rel. 34, Created)
DT
    01-OCT-1996 (Rel. 34, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
    Ovis aries (Sheep).
OS
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
    Bovidae; Caprinae; Ovis.
OX
    NCBI_TaxID=9940;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RX
    MEDLINE=95121932; PubMed=7821809;
КA
    Woodall C.J., McLaren L.J., Watt N.J.;
    "Sequence and chromosomal localisation of the gene encoding ovine
RT
    latent transforming growth factor-beta 1.";
RT
    Gene 150:371-373 (1994).
RL
RN
RP
    SEQUENCE OF 281-390 FROM N.A.
    STRAIN=Merino; TISSUE=Skin;
RC
RX
    MEDLINE=95268698; PubMed=7749621;
RA
    Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
```

```
RT
    "Growth factor expression in skin during wool follicle development.";
RL
    Comp. Biochem. Physiol. 110B:697-705(1995).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
    -!- SUBCELLULAR LOCATION: Secreted.
CC
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    -----
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    modified and this statement is not removed. Usage by and for commercial
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    or send an email to license@isb-sib.ch).
    _____
CC
DR
    EMBL; X76916; CAA54242.1; -.
DR
    EMBL; L36038; AAA31526.1; -.
DR
    PIR; 146463; 146463.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
DR
    Pfam; PF00688; TGFb propeptide; 1.
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
               1
    SIGNAL
                     23
                             POTENTIAL.
                     278
FT
    PROPEP
               24
                              POTENTIAL.
FT
    CHAIN
               279
                    390
                              TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
              285
                    294
                             BY SIMILARITY.
FT
                             BY SIMILARITY.
    DISULFID
              293
                    356
    DISULFID
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FT
              322
                    387
              326
                             BY SIMILARITY.
FT
    DISULFID
                     389
              355
                    355
FT
    DISULFID
                              INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
               82
                     82
FT
    CARBOHYD
              136
                    136
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FT
    CARBOHYD
              176
                    176
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                             CELL ATTACHMENT SITE (POTENTIAL).
FT
              244
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 Query Match
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 Best Local Similarity 90.6%; Pred. No. 1.7e-144;
 Matches 365; Conservative 10; Mismatches 15; Indels 13; Gaps
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Db

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Qу
            Db
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ΙD
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                 STANDARD:
                              PRT:
                                    390 AA. .
AC
    P01137; Q9UCG4;
DT
    21-JUL-1986 (Rel. 01, Created)
DT
    01-FEB-1991 (Rel. 17, Last sequence update)
    15-SEP-2003 (Rel. 42, Last annotation update)
DT
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DE
GN
    TGFB1 OR TGFB.
OS
    Homo sapiens (Human).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
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OX
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    MEDLINE=87174845; PubMed=3470709;
RX
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    Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
RT
    "Intron-exon structure of the human transforming growth factor-beta
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    precursor gene.";
RL
    Nucleic Acids Res. 15:3188-3189(1987).
RN
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    MEDLINE=85296301; PubMed=3861940;
RX
    Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
RA
    Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
RA
RT
    "Human transforming growth factor-beta complementary DNA sequence and
RT
    expression in normal and transformed cells.";
    Nature 316:701-705(1985).
RL
RN
RP
    SEQUENCE FROM N.A.
RC
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MEDLINE=22388257; PubMed=12477932;
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     Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA
     Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
     Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA
RA
     Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA
     Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
     Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
     Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA
RA
     Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
     Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA
     Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA
     Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA
RA
     Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA
     Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA
     Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
     Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA
     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA
RT
     "Generation and initial analysis of more than 15,000 full-length
RT
     human and mouse cDNA sequences.";
RL
     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
     [4]
     SEQUENCE OF 279-390 FROM N.A.
RP
RC
     TISSUE=Carcinoma;
RA
     Urushizaki Y., Niitsu Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
RA
     Urushizaki I., Takahashi Y., Ito H.;
     "Cloning and expression of the gene for human transforming growth
RT
RT
     factor-beta in Escherichia coli.";
     Tumor Res. 22:41-55(1987).
RL
RN
     [5]
RP
     SEQUENCE OF 279-329.
RC
     TISSUE=Bladder carcinoma;
RX
     MEDLINE=93229900; PubMed=8471846;
     Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,
RA
RA
     Hu S., Westcott K.R.;
     "Recombinant human transforming growth factor-beta 1: expression by
RT
RT
     Chinese hamster ovary cells, isolation, and characterization.";
RL
     Protein Expr. Purif. 4:130-140(1993).
RN
     [6]
     SEQUENCE OF 279-301.
RP
RX
     MEDLINE=85131019; PubMed=2982829;
RA
     Massague J., Like B.;
RT
     "Cellular receptors for type beta transforming growth factor. Ligand
RT
     binding and affinity labeling in human and rodent cell lines.";
RL
     J. Biol. Chem. 260:2636-2645(1985).
RN
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     Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA
RA
     Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA
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RT
     "Transforming growth factor beta 1: NMR signal assignments of the
RT
     recombinant protein expressed and isotopically enriched using Chinese
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     Biochemistry 32:1152-1163(1993).
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RA
     Torchia D.A.;
RT
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RL
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RN
RΡ
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RA
     Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
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RA
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RA
RT
     "Transforming growth factor beta 1: three-dimensional structure in
RT
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RT
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RL
     Biochemistry 35:8517-8534(1996).
CC
     -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC
         DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC
         CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC
         SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC
         ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
         POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
     -!- SUBUNIT: Homodimer; disulfide-linked.
CC
     -!- SUBCELLULAR LOCATION: Secreted.
CC
     -!- SIMILARITY: Belongs to the TGF-beta family.
CC
     CC
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     use by non-profit institutions as long as its content is in no way
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     or send an email to license@isb-sib.ch).
CC
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DR
     EMBL; X05839; CAA29283.1; -.
DR
     EMBL; X05840; CAA29283.1; JOINED.
DR
     EMBL; X05843; CAA29283.1; JOINED.
     EMBL; X05844; CAA29283.1; JOINED.
DR
DR
     EMBL; X05849; CAA29283.1; JOINED.
DR
     EMBL; X05850; CAA29283.1; JOINED.
DR
     EMBL; X02812; CAA26580.1; ALT SEQ.
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DR
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DR
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DR
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DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb_N.
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    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
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    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
    Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure.
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FT
    PROPEP
                24
                      278
FT
    CHAIN
               279
                      390
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FT
    DISULFID
                      294
               285
FT
    DISULFID
               293
                      356
FT
    DISULFID
               322
                      387
FT
    DISULFID
               326
                      389
FT
               355
    DISULFID
                      355
                               INTERCHAIN.
FT
    CARBOHYD
                       82
                82
                               N-LINKED (GLCNAC. . .) (POTENTIAL) .
                               N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
                      136
               136
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FT
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               176
                      176
FT
    SITE
               244
                      246
                               CELL ATTACHMENT SITE (POTENTIAL).
                               L \rightarrow P (IN REF. 2).
FT
    CONFLICT
                10
                       10
FT
    CONFLICT
               159
                      159
                               R \rightarrow RR (IN REF. 2).
FT
    STRAND
               281
                      281
FT
    TURN
               282
                      287
FT
    STRAND
               294
                      296
FT
    STRAND
               300
                      300
FT
    TURN
               302
                      305
FT
    STRAND
               313
                      313
FT
               317
    STRAND
                      317
FT
    STRAND
               321
                      323
    HELIX
               335
FT
                      346
FT
    TURN
                      349
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FT
    STRAND
               358
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    TURN
               371
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FT
    STRAND
               373
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    SEQUENCE
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                      44341 MW;
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 Best Local Similarity 90.6%; Pred. No. 1.8e-143;
 Matches 365; Conservative 10; Mismatches
                                             15;
                                                  Indels
                                                           13; Gaps
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Qу
             Db
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Db
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Pfam; PF00019; TGF-beta; 1.

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Qу
             288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
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Qу
             Dh
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    01-MAR-1989 (Rel. 10, Created)
    01-MAR-1989 (Rel. 10, Last sequence update)
DT
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Transforming growth factor beta 1 precursor (TGF-beta 1).
DE
GN
    TGFB1.
    Cercopithecus aethiops (Green monkey) (Grivet).
OS
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
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OC
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RX
    MEDLINE=87246074; PubMed=3474130;
    Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
RA
RT
    "Cloning and sequence analysis of simian transforming growth
RT
    factor-beta cDNA.";
RL
    DNA 6:239-244(1987).
CC
    -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION,
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
        CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE
CC
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    -----
CC
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    or send an email to license@isb-sib.ch).
CC
    EMBL; M16658; AAA35369.1; -.
DR
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DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
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InterPro; IPR001839; TGFb.
DR
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DR
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    Pfam; PF00688; TGFb_propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DΡ
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
FT
    SIGNAL
                     16
                             POTENTIAL.
               1
FT
    PROPEP
                    278
               17
FT
    CHAIN
              279
                    390
                             TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
              285
                    294
                            BY SIMILARITY.
FT
    DISULFID
              293
                    356
                            BY SIMILARITY.
                    387
FT
    DISULFID
              322
                            BY SIMILARITY.
    DISULFID
              326
                    389
                            BY SIMILARITY.
FT
FT
    DISULFID
              355
                    355
                             INTERCHAIN (BY SIMILARITY).
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
                    82
              82
FT
    CARBOHYD
              136
                    136
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              176
                    176
FT
    SITE
              244
                    246
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                      89.6%; Score 1916.5; DB 1; Length 390;
 Best Local Similarity 90.3%; Pred. No. 2.5e-143;
 Matches 364; Conservative 10; Mismatches
                                         16; Indels
                                                      13; Gaps
                                                                 1;
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Qу
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Qу
            Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            Db
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DR

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RESULT 5
TGF1 CANFA
    TGF1 CANFA
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                                PRT; 390 AA.
AC
    P54831;
DT
    01-OCT-1996 (Rel. 34, Created)
DT
    01-OCT-1996 (Rel. 34, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DΕ
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
OS
    Canis familiaris (Dog).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX
    NCBI TaxID=9615;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Jugular vein endothelial;
RX
    MEDLINE=95237630; PubMed=7721110;
    Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;
RA
RT
    "Cloning of a canine cDNA homologous to the human transforming growth
    factor-beta 1-encoding gene.";
RT
RL
    Gene 155:307-308(1995).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
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CC
CC
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    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
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CC
    or send an email to license@isb-sib.ch).
CC
    DR
    EMBL; L34956; AAA51458.1; -.
DR
    PIR; JC4023; JC4023.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF_cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB: 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
                            POTENTIAL.
FT
    SIGNAL
                1 23
    PROPEP
                      278
FT
                24
                               BY SIMILARITY.
FT
    CHAIN
               279
                     390
                              TRANSFORMING GROWTH FACTOR BETA 1.
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FT
    DISULFID
              285
                    294
                            BY SIMILARITY.
FT
    DISULFID
              293
                    356
                            BY SIMILARITY.
FT
    DISULFID
              322
                    387
                            BY SIMILARITY.
FT
    DISULFID
              326
                    389
                            BY SIMILARITY.
FT
    DISULFID
              355
                    355
                             INTERCHAIN.
FT
    CARBOHYD
               82
                     82
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
              136
                    136
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
              176
                    176
FT
    SITE
                            CELL ATTACHMENT SITE (POTENTIAL).
              244
                    246
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SO
             390 AA; 44185 MW; EB4780E88B7B590E CRC64;
 Query Match
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 Best Local Similarity 89.6%; Pred. No. 1.1e-141;
 Matches 361; Conservative 12; Mismatches 17; Indels
                                                      13; Gaps
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Db
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        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEOHVELYOKYSNDSWR 180
Qу
            Dh
        121 YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLKLKAEQHVELYQKYSNDSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
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Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
            Db
        241 SSRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRORR------ALDTNYCFS 287
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHN 347
Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
            Db
        348 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 6
TGF1 HORSE
    TGF1 HORSE
ID
                STANDARD;
                             PRT;
                                   390 AA.
AC
    019011;
DT
    15-JUL-1998 (Rel. 36, Created)
DT
    15-JUL-1998 (Rel. 36, Last sequence update)
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
OS
    Equus caballus (Horse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX
    NCBI TaxID=9796;
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RN
     [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Lymph node;
RX
    MEDLINE=98185507; PubMed=9524819;
RA
    Penha-Goncalves M.N., Onions D.E., Nicolson L.;
RT
     "Cloning and sequencing of equine transforming growth factor-beta 1
RT
     (TGF beta-1) cDNA.";
RL
    DNA Seq. 7:375-378(1997).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
CC
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CC
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CC
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    modified and this statement is not removed. Usage by and for commercial
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CC
    or send an email to license@isb-sib.ch).
CC
DR
    EMBL; X99438; CAA67801.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FΤ
    SIGNAL
                1
                      23
                             POTENTIAL.
FT
    PROPEP
                24
                      278
                               BY SIMILARITY.
FT
                279
                      390
                               TRANSFORMING GROWTH FACTOR BETA 1.
    CHAIN
FT
    DISULFID
              285 294
                              BY SIMILARITY.
FT
    DISULFID
             293 356
                              BY SIMILARITY.
FT
    DISULFID
               322
                     387
                               BY SIMILARITY.
FT
    DISULFID
               326
                     389
                               BY SIMILARITY.
    DISULFID 355
FT
                     355
                               INTERCHAIN (BY SIMILARITY).
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
                82
                      82
                     136
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD 136
              176 176
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
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 Query Match
                        86.1%; Score 1841.5; DB 1; Length 390;
 Best Local Similarity 87.3%; Pred. No. 2e-137;
 Matches 352; Conservative 12; Mismatches 26; Indels 13; Gaps
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         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
Qу
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Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
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QУ
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Db
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
QУ
            Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            Db
        348 PGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 7
TGF1 MOUSE
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                STANDARD;
                             PRT;
                                   390 AA.
AC
    P04202;
    20-MAR-1987 (Rel. 04, Created)
DT
DT
    20-MAR-1987 (Rel. 04, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
OS
    Mus musculus (Mouse).
OC.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Mus.
OC.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=86168129; PubMed=3007454;
RA
    Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT
    "The murine transforming growth factor-beta precursor.";
    J. Biol. Chem. 261:4377-4379(1986).
RL
RN
    SEOUENCE FROM N.A.
RP
RC
    STRAIN=BALB/C;
RX
    MEDLINE=96096545; PubMed=8522200;
RA
    Guron C., Sudarshan C., Raghow R.;
RT
    "Molecular organization of the gene encoding murine transforming
RT
    growth factor beta 1.";
RL
    Gene 165:325-326(1995).
RN
    [3]
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RР
     SEQUENCE FROM N.A.
RC
     STRAIN=C57BL/6, and NOD/LT; TISSUE=Spleen;
RA
     Poirot L., Benoist C., Mathis D.;
     "Transforming growth factor-beta 1 sequence and expression: no
RT
RT
     difference between NOD/Lt and C57Bl/6 mouse strains.";
RL
     Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
CC
     -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
         PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
         TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
         HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
         A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
     -!- SUBUNIT: Homodimer; disulfide-linked.
CC
     -!- SUBCELLULAR LOCATION: Secreted.
CC
     -!- SIMILARITY: Belongs to the TGF-beta family.
CC
     -----
CC
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CC
     EMBL; M13177; AAA40423.1; -.
DR
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DR
     EMBL; L42456; AAB00138.1; JOINED.
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     EMBL; L42457; AAB00138.1; JOINED.
     EMBL; L42458; AAB00138.1; JOINED.
DR
DR
     EMBL; L42459; AAB00138.1; JOINED.
     EMBL; L42460; AAB00138.1; JOINED.
DR
     EMBL; L42461; AAB00138.1; JOINED.
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DR
     EMBL; AJ009862; CAA08900.1; -.
DR
    PIR; A01396; WFMS2.
DR
    HSSP; P01137; 1KLA.
DR
    MGD; MGI:98725; Tgfb1.
DR
    GO; GO:0005578; C:extracellular matrix; IDA.
DR
    GO; GO:0006954; P:inflammatory response; IMP.
    GO; GO:0007515; P:lymph gland development; IMP.
DR
DR
    GO; GO:0008220; P:necrosis; IMP.
DR
    GO; GO:0016202; P:regulation of myogenesis; IDA.
DR
    InterPro; IPR002400; GF_cysknot.
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     InterPro; IPR003911; TGF_TGFb.
DR
     InterPro; IPR001839; TGFb.
DR
     InterPro; IPR001111; TGFb N.
DR
     Pfam; PF00019; TGF-beta; \overline{1}.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
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                        23
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FT
    PROPEP
                 24
                       278
FT
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                279
                       390
                                TRANSFORMING GROWTH FACTOR BETA 1.
FT
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                                BY SIMILARITY.
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FT
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              293
                    356
                             BY SIMILARITY.
FT
    DISULFID
              322
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                             BY SIMILARITY.
FT
    DISULFID
              326
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                             BY SIMILARITY.
FT
    DISULFID
              355
                    355
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FT
    CARBOHYD
               82
                     82
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    CARBOHYD
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
              136
                    136
FT
    CARBOHYD
              176
                    176
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
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              244
SQ
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 Query Match
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 Best Local Similarity 85.9%; Pred. No. 4.1e-137;
 Matches 346; Conservative 15; Mismatches
                                           29; Indels
                                                       13; Gaps
                                                                  1:
Qу
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            1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
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Db
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Db
        181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
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Db
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Db
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            Db
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Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
            Db
        348 PGASASPCCVPOALEPLPIVYYVGRKPKVEOLSNMIVRSCKCS 390
RESULT 8
TGF1 RAT
ID
    TGF1 RAT
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                                    390 AA.
AC
    P17246;
DT
    01-AUG-1990 (Rel. 15, Created)
DT
    01-AUG-1990 (Rel. 15, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
    TGFB1.
OS
    Rattus norvegicus (Rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
    NCBI TaxID=10116;
RN
    [1]
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RΡ
    SEQUENCE FROM N.A.
RC
    STRAIN=Sprague-Dawley; TISSUE=Heart;
RX
    MEDLINE=90272425; PubMed=2349108;
    Qian S.W., Kondaiah P., Roberts A.B., Sporn M.B.;
RA
    "cDNA cloning by PCR of rat transforming growth factor beta-1.";
RT
RL
    Nucleic Acids Res. 18:3059-3059(1990).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    CC
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    or send an email to license@isb-sib.ch).
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CC
    EMBL; X52498; CAA36741.1; -.
DR
DR
    PIR; S10219; S10219.
DR
    HSSP; P01137; 1KLA.
    InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                1
                      23
                               POTENTIAL.
FT
    PROPEP
                      278
                24
    CHAIN
FT
               279
                      390
                             TRANSFORMING GROWTH FACTOR BETA 1.
                             BY SIMILARITY.
FT
    DISULFID
               285
                      294
FT
    DISULFID
             293 356
                              BY SIMILARITY.
FT
    DISULFID
             322 387
                              BY SIMILARITY.
FT
    DISULFID
              326
                     389
                              BY SIMILARITY.
FT
    DISULFID
              355
                     355
                               INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
               82
                      82
FT
    CARBOHYD
               136
                      136
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FT
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               176
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                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
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                     246
                              CELL ATTACHMENT SITE (POTENTIAL).
SO
    SEQUENCE 390 AA; 44329 MW; 5E21108ED50D853C CRC64;
 Query Match
                        85.9%; Score 1837.5; DB 1; Length 390;
 Best Local Similarity 85.9%; Pred. No. 4.1e-137;
 Matches 346; Conservative 14; Mismatches 30; Indels 13; Gaps
                                                                        1;
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Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
            Dh
          1 MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
            Db
         61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNDSWR 180
QУ
            Db
        121 YDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
Db
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
             Db
        241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR------ALDTNYCFS 287
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
            288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
Qу
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
            Dh
        348 PGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
RESULT 9
TGF1 CAVPO
    TGF1 CAVPO
                STANDARD;
                             PRT:
                                   390 AA.
AC
    Q9Z1Y6; Q9QZB3; Q9R148;
DT
    16-OCT-2001 (Rel. 40, Created)
DT
    16-OCT-2001 (Rel. 40, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1).
GN
OS
    Cavia porcellus (Guinea pig).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC
OX
    NCBI TaxID=10141;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Hartley;
RA
    Jeevan A., McMurray D.N., Yoshimura T.;
RT
    "Guinea pig transforming growth factor-beta in peritoneal exudates
RT
    after BCG vaccination.";
    Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RL
RN
    [2]
RΡ
    SEQUENCE OF 265-382 FROM N.A.
RX
    MEDLINE=99144670; PubMed=10025978;
    Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RA
RT
    "Spontaneous cytokine gene expression in normal quinea pig blood and
RT
    tissues.";
    Cytokine 10:851-859(1998).
RL
RN
    [3]
```

```
RP
    SEQUENCE OF 279-371 FROM N.A.
RC
    STRAIN=Hartley; TISSUE=Trachea;
RA
    Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
RA
    Sekizawa K.;
RT
     "Guinea-pig transforming growth factor-beta expression in injured
RT
    tracheal epithelium.";
RL
    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC
     -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC
        DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC
        CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC
        SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC
        POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
    ------
CC
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CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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    the European Bioinformatics Institute. There are no restrictions on its
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    use by non-profit institutions as long as its content is in no way
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    modified and this statement is not removed. Usage by and for commercial
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    or send an email to license@isb-sib.ch).
CC
    ______
    EMBL; AF191297; AAF02780.1; -.
DR
    EMBL; AF097509; AAC83807.1; -.
DR
DR
    EMBL; AF169347; AAD49347.1; -.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FΤ
    SIGNAL
                 1
                       24
                                POTENTIAL.
FT
    PROPEP
                25
                       278
                                POTENTIAL.
FT
    CHAIN
                279
                       390
                               TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
                285
                      294
                               BY SIMILARITY.
FT
    DISULFID
                293
                      356
                               BY SIMILARITY.
FT
    DISULFID
                                BY SIMILARITY.
                322
                       387
FΤ
    DISULFID
                326
                      389
                                BY SIMILARITY.
FT
    DISULFID
                355
                     355
                                INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
                      82
                82
                                N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               136
                     136
                                N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               176
                      176
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    SITE
               244
                      246
                               CELL ATTACHMENT SITE (POTENTIAL).
FT
    CONFLICT
               279
                      279
                               G \rightarrow P (IN REF. 3).
FT
    CONFLICT
                286
                      286
                                F -> S (IN REF. 2).
FT
    CONFLICT
                309
                      309
                                K \rightarrow E (IN REF. 2).
FT
    CONFLICT
                322
                      322
                               C \rightarrow R (IN REF. 2).
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FT
             350
    CONFLICT
                  350
                           A \rightarrow G (IN REF. 2).
SO
             390 AA; 44328 MW; 1539F849BA0C0FF1 CRC64:
    SEQUENCE
                      85.5%; Score 1828.5; DB 1; Length 390;
 Query Match
                     85.6%; Pred. No. 2.1e-136;
 Best Local Similarity
 Matches 345; Conservative 15; Mismatches
                                          30;
                                              Indels
                                                      13; Gaps
                                                                 1;
Qу
          1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
            1 MPPSRLRLLPLLLPLLWLLVLAPGRPASGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Db
Qу
         61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOI 120
            61 SPPSOGDVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEPDYYAKEVTRVLMVDNSHNI 120
Db
        121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
                  Db
        121 YKSIETVAHSIYMFFNTSELREAVPDPLLLSRAELRMORLKLNVEOHVELYOKYSNNSWR 180
        181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
            Db
        181 YLSNQLLTPSDTPEWLSFDVTGVVROWLSOGEELEGFRFSAHCSCDSKDNTLRVEINGIG 240
        241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
              Db
        241 PKRRGDLAAIHGMNRPFLLLMATPLERAQHLHSSRHRR------GLDTNYCFS 287
        301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNOHN 360
Qy
            Db
        288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
        361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            Db
        348 PGASAAPCCVPOALEPLPIVYYVGRKAKVEOLSNMIVRSCKCS 390
RESULT 10
TGF1 BOVIN
    TGF1 BOVIN
                STANDARD:
                             PRT:
                                   315 AA.
AC
    P18341;
    01-NOV-1990 (Rel. 16, Created)
DT
DT
    01-NOV-1990 (Rel. 16, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
    TGFB1.
GN
OS
    Bos taurus (Bovine).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
    Bovidae; Bovinae; Bos.
OC
    NCBI TaxID=9913;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
    MEDLINE=91042552; PubMed=3153459;
RX
RA
    van Obberghen-Schilling E., Kondaiah P., Ludwig R.L., Sporn M.B.,
RA
    Baker C.C.:
RT
    "Complementary deoxyribonucleic acid cloning of bovine transforming
RT
    growth factor-beta 1.";
```

```
RL
    Mol. Endocrinol. 1:693-698(1987).
RN
    [2]
RP
    SUBUNITS.
RC
    TISSUE=Bone;
RX
    MEDLINE=92129307; PubMed=1733936;
RA
    Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
RT
    "Purification and characterization of transforming growth factor-beta
RT
    2.3 and -beta 1.2 heterodimers from bovine bone.";
RL
    J. Biol. Chem. 267:2325-2328(1992).
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked. Heterodimers of TGF-beta 1/2
CC
        have been found in bone.
    -!- SUBCELLULAR LOCATION: Secreted.
CC
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
    CC
CC
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    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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    the European Bioinformatics Institute. There are no restrictions on its
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    or send an email to license@isb-sib.ch).
CC
    DR
    EMBL; M36271; AAA30778.1; -.
DR
    PIR; A40057; A40057.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein.
FT
    NON TER
              1
                       1
    PROPEP
FT
                <1
                      203
FT
               204
    CHAIN
                      315
                               TRANSFORMING GROWTH FACTOR BETA 1.
FT
    DISULFID
              210
                      219
                               BY SIMILARITY.
             218
FT
    DISULFID
                    281
                               BY SIMILARITY.
             247
                   312
FT
    DISULFID
                              BY SIMILARITY.
FT
    DISULFID 251 314
                              BY SIMILARITY.
    DISULFID 280 280
FT
                              INTERCHAIN (BY SIMILARITY).
FΤ
    CARBOHYD
               7
                      7
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               61
                     61
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
             101
                     101
              169 171
                           CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
             315 AA; 36269 MW; C2717A23D994E00E CRC64;
SO
    SEOUENCE
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Best Local Similarity 89.9%; Pred. No. 1.5e-116;
 Matches 295; Conservative 9; Mismatches 11; Indels
                                                       13: Gaps
                                                                  1;
Qу
         76 AVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
            Db
          1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60
        136 NTSELREAVPEPVLLSRAELRLKLKKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
Qу
            61 NTSELREAVPEPVLLSRADVRLLRLKLKVEOHVELYOKYSNNSWRYLSNRLLAPSDSPEW 120
Db
        196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
Qу
            121 LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR 180
Db
        256 PFLLLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVROLYIDF 315
Ov
            181 PFLLLMATPLERAOHLHSSRHRR-----ALDTNYCFSSTEKNCCVROLYIDF 227
Db
        316 RKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTOYSKVLALYNOHNPGASAAPCCVPOALE 375
Qу
            Db
        228 RKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALE 287
        376 PLPIVYYVGRKPKVEOLSNMIVRSCKCS 403
Qу
            Db
        288 PLPIVYYVGRKPKVEQLSNMIVRSCKCS 315
RESULT 11
TGF1 CHICK
    TGF1 CHICK
                 STANDARD;
                              PRT;
                                    373 AA.
AC
    P09531;
    01-MAR-1989 (Rel. 10, Created)
DT
DT
    01-OCT-1996 (Rel. 34, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 4)
DE
    (Fragment).
GN
    TGFB1.
OS
    Gallus gallus (Chicken).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC
    Gallus.
    NCBI TaxID=9031;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
    STRAIN=White leghorn;
RC
    MEDLINE=89112198; PubMed=2464131;
RX
RA
    Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT
    "Complementary deoxyribonucleic acid cloning of a messenger
RT
    ribonucleic acid encoding transforming growth factor beta 4 from
RT
    chicken embryo chondrocytes.";
RL
    Mol. Endocrinol. 2:1186-1195(1988).
RN
    [2]
RP
    REVISIONS.
RX
    MEDLINE=92357039; PubMed=1353860;
    Burt D.W., Jakowlew S.B.;
```

73.6%; Score 1574.5; DB 1; Length 315;

Query Match

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RT
    "Correction: a new interpretation of a chicken transforming growth
RT
    factor-beta 4 complementary DNA.";
    Mol. Endocrinol. 6:989-992(1992).
RL
CC
    -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC
        HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC
        ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC
        A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
     CC
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    or send an email to license@isb-sib.ch).
     CC
DR
    EMBL; M31160; AAB05637.1; -.
DR
    PIR; A41918; A41918.
DR
    HSSP; P01137; 1KLA.
DR
    InterPro; IPR003911; TGF TGFb.
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    NON TER
                1
                        1
                <1
FT
    SIGNAL
                        1
                               POTENTIAL.
FT
    PROPEP
                2
                      259
                               POTENTIAL.
FT
    CHAIN
               260
                      373
                               TRANSFORMING GROWTH FACTOR BETA 1.
               266
FT
    DISULFID
                      277
                              BY SIMILARITY.
                              BY SIMILARITY.
FT
    DISULFID
               276
                      339
                              BY SIMILARITY.
FT
    DISULFID
               305
                      370
FT
    DISULFID
               309
                      372
                               BY SIMILARITY.
FT
               338
                      338
    DISULFID
                               INTERCHAIN (BY SIMILARITY).
FT
    CARBOHYD
               54
                      54
                               N-LINKED (GLCNAC. . .) (POTENTIAL) .
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               109
                      109
FT
    CARBOHYD
              153
                      153
                               N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
    SITE
               224
                      226
                               CELL ATTACHMENT SITE (POTENTIAL).
SQ
    SEQUENCE
              373 AA; 42634 MW; 9903F3479C8552E5 CRC64;
 Query Match
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 Best Local Similarity 53.5%; Pred. No. 3.9e-75;
 Matches 207; Conservative 52; Mismatches 100; Indels
                                                           28; Gaps
                                                                       8:
Qу
          30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
             Db
           2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
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90 GES-VEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
Qу
              62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
Db
         149 LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
Qу
                              121 LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
Db
         204 VROWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
Qу
            181 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239
Dh
         259 LLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYCF--SSTEKNCCVROLYIDFR 316
QУ
            240 LAMALPAERANELHSARRRR------DLDTDYCFGPGTDEKNCCVRPLYIDFR 286
Db
        317 KDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEP 376
Qу
            Db
         287 KDLQWKWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGASAAPCCVPOTLDP 346
        377 LPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            Db
        347 LPIIYYVGRNVRVEQLSNMVVRACKCS 373
RESULT 12
TGF1 XENLA
ID
    TGF1 XENLA
                 STANDARD;
                                     382 AA.
                               PRT;
AC
    P16176;
DT
    01-APR-1990 (Rel. 14, Created)
DT
    01-APR-1990 (Rel. 14, Last sequence update)
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DE
    Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 5).
OS
    Xenopus laevis (African clawed frog).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC
    Xenopodinae; Xenopus.
OX
    NCBI TaxID=8355;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RX
    MEDLINE=90110090; PubMed=2295601;
RA
    Kondaiah P., Sands M.J., Smith J.M., Fields A., Roberts A.B.,
RA
    Sporn M.B., Melton D.A.;
RT
    "Identification of a novel transforming growth factor-beta (TGF-beta
RT
    5) mRNA in Xenopus laevis.";
    J. Biol. Chem. 265:1089-1093(1990).
RL
RN
    [2]
    SEQUENCE FROM N.A.
ŘΡ
    Vempati U.D., Kondaiah P.;
RA
RL
    Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: IMPORTANT ROLE IN CERTAIN ASPECTS OF DIFFERENTIATION.
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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    or send an email to license@isb-sib.ch).
CC
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    EMBL; J05180; AAA49968.1; -.
DR
    EMBL; AF009335; AAB64441.1; -.
DR
    EMBL; AF009331; AAB64441.1; JOINED.
DR
    EMBL; AF009332; AAB64441.1; JOINED.
DR
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    EMBL; AF009334; AAB64441.1; JOINED.
DR
    PIR; A34929; B61036.
DR
    HSSP; P01137; 1KLA.
DR
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
    SIGNAL
                1
                      21
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FT
    PROPEP
                      270
                22
FT
                     382
    CHAIN
               271
                             TRANSFORMING GROWTH FACTOR BETA 1.
FT
             277
                     286
                             BY SIMILARITY.
    DISULFID
FT
    DISULFID
             285 348
                             BY SIMILARITY.
FT
    DISULFID
             314
                     379
                             BY SIMILARITY.
             318
FT
    DISULFID
                     381
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             347
                   347
FT
    DISULFID
                              INTERCHAIN (BY SIMILARITY).
    CARBOHYD
FT
               73
                      73
                             N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
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 Matches 190; Conservative 55; Mismatches 122; Indels 43; Gaps
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           9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
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           1 MEVLWMLLVLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKTPDV-DS 59
          69 PPGPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDK 123
Qу
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          60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED- 115
         124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEQHVELYQKYSNDSW-- 179
Qу
                 Db
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QУ
         180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
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Db
         171 SRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEOFGLOPACKCPTPQAKD----ID 226
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Qу
                    11111::
                                Db
         227 IEGF-PALRGDLASLSSKENTKPYLMITSMPAERIDTVTSSRKKR------GV 272
         294 DTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVL 353
Qу
                       Db
         273 GQEYCFGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQYSKVL 332
         354 ALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
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         333 SLYNONNPGASISPCCVPDVLEPLPIIYYVGRTAKVEOLSNMVVRSCNCS 382
RESULT 13
TGF3 CHICK
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                                PRT; 412 AA.
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    P16047;
    01-APR-1990 (Rel. 14, Created)
DT
    16-OCT-2001 (Rel. 40, Last sequence update)
DT
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Transforming growth factor beta 3 precursor (TGF-beta 3).
GN
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OS
    Gallus gallus (Chicken).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
    Gallus.
OC
    NCBI TaxID=9031;
OX
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RP
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    MEDLINE=89096966; PubMed=3211158;
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RA
    Jakowlew S.B., Dillard P.J., Kondaiah P., Sporn M.B., Roberts A.B.;
RT
    "Complementary deoxyribonucleic acid cloning of a novel transforming
RT
    growth factor-beta messenger ribonucleic acid from chick embryo
RT
    chondrocytes.":
RL
    Mol. Endocrinol. 2:747-755(1988).
    [2]
RN
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=White leghorn;
RX
    MEDLINE=95169270; PubMed=7865129;
RA
    Burt D.W., Dey B.R., Paton I.R., Morrice D.R., Law A.S.;
RT
    "The chicken transforming growth factor-beta 3 gene: genomic
RT
    structure, transcriptional analysis, and chromosomal location.";
RL
    DNA Cell Biol. 14:111-123(1995).
RN
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RΡ
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    STRAIN=White leghorn; TISSUE=Blood;
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    MEDLINE=92134496; PubMed=1840616;
RA
    Burt D.W., Dey B.R., Paton I.R.;
    "Comparative analysis of human and chicken transforming growth
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    factor-beta 2 and -beta 3 promoters.";
    J. Mol. Endocrinol. 7:175-183(1991).
RL
RN
    [4]
    SEQUENCE OF 1-117 FROM N.A.
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    MEDLINE=93024487; PubMed=1406706;
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RA
    Jakowlew S.B., Lechleider R., Geiser A.G., Kim S.J.,
RA
    Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;
RT
    "Identification and characterization of the chicken transforming
RT
    growth factor-beta 3 promoter.";
RL
    Mol. Endocrinol. 6:1285-1298(1992).
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC
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    or send an email to license@isb-sib.ch).
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    EMBL; X60090; CAA41128.2; JOINED.
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DR
    InterPro; IPR003911; TGF_TGFb.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
    PRINTS; PR01423; TGFBETA.
DR
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
    Growth factor; Mitogen; Glycoprotein; Signal.
FT
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                1
                       23
                               POTENTIAL.
FT
    PROPEP
                24
                      300
FΤ
    CHAIN
                301
                      412
                               TRANSFORMING GROWTH FACTOR BETA 3.
               307
FT
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                      316
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               315
                    378
                              BY SIMILARITY.
FT
    DISULFID
               344
                    409
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FT
    DISULFID
               348
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FT
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               377
                     377
                                INTERCHAIN (BY SIMILARITY).
FT
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                74
                       74
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FT
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               135
                     135
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               142
                      142
                               N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
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               261
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                               CELL ATTACHMENT SITE (POTENTIAL).
FT
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               323
                      326
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 Best Local Similarity 45.9%; Pred. No. 8.7e-60;
 Matches 195; Conservative 56; Mismatches 117; Indels 57; Gaps
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Db
         75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNQIYDKF 124
Qу
              :||||||||::||::||::|
                                                        | : :
Db
         67 YQILALYNSTRELL--EEMEEEKEESCSQENTESEYYAKEIHKFDMIOGLPEHNELGICP 124
         125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND--- 177
Qу
               ::: || |
                                 : || :||:
        125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180
Db
         178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
QУ
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Db
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QУ
               | :: | :|
                            241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR 300
Db
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Qу
                       Db
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Qу
            Db
        348 CPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 407
        399 SCKCS 403
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            Db
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RESULT 14
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AC
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DT
    01-APR-1990 (Rel. 14, Created)
    01-APR-1990 (Rel. 14, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DΤ
DE
    Transforming growth factor beta 3 precursor (TGF-beta 3).
GN
    TGFB3.
OS
    Sus scrofa (Pig).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX
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RN
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RC
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RX
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RA
    Derynck R., Lindquist B., Lee A., Wen D., Tamm J., Graycar J.L.,
RA
    Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,
RA
    Chen E.Y.;
RT
    "A new type of transforming growth factor-beta, TGF-beta 3.";
    EMBO J. 7:3737-3743 (1988).
RL
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
    -!- SUBUNIT: Homodimer; disulfide-linked.
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CC
    -!- SUBCELLULAR LOCATION: Secreted.
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
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CC
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DR
    PIR; S01825; S01825.
DR
    HSSP; P10600; 1TGJ.
DR
DR
    InterPro; IPR002400; GF cysknot.
    InterPro; IPR003911; TGF TGFb.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
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FT
    SIGNAL 1 18
                            POTENTIAL.
FΤ
    PROPEP
                       297
                19
               298 409 TRANSFORMING GROWTH FACTOR BETA 3.
304 313 BY SIMILARITY.
FT
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FT
    DISULFID 304 313
FT
    DISULFID 312 375
                              BY SIMILARITY.
   DISULFID 345 408 BY SIMILARITY.

DISULFID 374 374 INTERCHAIN (BY SIMILARITY).

CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT
    SITE 259 261 CELL ATTACHMENT SITE (POTENTIAL).
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Db
Qу
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               65 TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124
Db
         127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
Qу
                 125 ITSKIFR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180
Db
         179 WRYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAH-----SSSDSKDN- 230
QУ
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Db
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Qу
                          : :: | :|
         241 OEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLILMMIPPDRLDNPGLGAORKKR--- 297
Db
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Qу
                     298 -----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPY 347
Dh
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Qу
            Db
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        402 CS 403
QУ
           - 11
        408 CS 409
Db
RESULT 15
TGF3 MOUSE
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AC
    P17125;
DT
    01-AUG-1990 (Rel. 15, Created)
    01-AUG-1990 (Rel. 15, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DE
    Transforming growth factor beta 3 precursor (TGF-beta 3).
GN
    TGFB3.
    Mus musculus (Mouse).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
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OX
RN
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RΡ
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    MEDLINE=90190650; PubMed=2628730;
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    Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.;
RA
RT
    "Complementary DNA cloning of the murine transforming growth
RT
    factor-beta 3 (TGF beta 3) precursor and the comparative expression
RT
    of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
RT
    adult tissues.";
    Mol. Endocrinol. 3:1926-1934(1989).
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    MEDLINE=91000714; PubMed=2206556;
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    Denhez F., Lafyatis R., Kondaiah P., Roberts A.B., Sporn M.B.;
RT
    "Cloning by polymerase chain reaction of a new mouse TGF-beta,
RT
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    Growth Factors 3:139-146(1990).
RL
CC
    -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC
    -!- SUBUNIT: Homodimer; disulfide-linked.
    -!- SUBCELLULAR LOCATION: Secreted.
CC
CC
    -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC
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CC
DR
    EMBL; M32745; AAA40422.1; -.
DR
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    HSSP; P10600; 1TGJ.
DR
    MGD; MGI:98727; Tgfb3.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    InterPro; IPR001839; TGFb.
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    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 1.
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DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
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    SMART; SM00204; TGFB; 1.
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DR
    PROSITE; PS00250; TGF BETA 1; 1.
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
             1
                    23
FT
    SIGNAL
                            POTENTIAL.
    PROPEP
              24
                    298
                             POTENTIAL.
FT
FT
    CHAIN
              299
                   410
                            TRANSFORMING GROWTH FACTOR BETA 3.
FT
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                   314
                           BY SIMILARITY.
    DISULFID 313 376
DISULFID 342 407
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BY SIMILARITY.
BY SIMILARITY.
FT
FT
FT
    DISULFID 375 375
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FT
                           N-LINKED (GLCNAC. . .) (POTENTIAL) .
    CARBOHYD 72
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    CARBOHYD 133 133
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FT
                           N-LINKED (GLCNAC. . .) (POTENTIAL) .
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             259 261
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 Matches 188; Conservative 58; Mismatches 126; Indels 49; Gaps
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            Db
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         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG 126
             65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
Db
Qу
        127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
               Db
        125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
        179 WRYLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Ov
             : | :|
        181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV 240
Db
        231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAOHLHSSRHRRALDT 282
QУ
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CC

Db	241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRK 296
Qy	283 NDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYI 342 : : : : : : :
Db	297KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYL 349
Qу	343 WSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC 402
Db	350 RSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKC 409
Qy	403 S 403
Db	410 S 410

Db

Search completed: October 28, 2003, 09:08:41

Job time : 9.07747 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 07:50:55; Search time 32.3099 Seconds

(without alignments)

3218.683 Million cell updates/sec

US-10-017-372E-33 Title:

Perfect score: 2139

1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 403 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

830525 seqs, 258052604 residues Searched:

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*

> 1: sp archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp human:*

5: sp_invertebrate:*

6: sp_mammal:* 7: sp_mhc:* 8: sp_organelle:*
9: sp_phage:*

10: sp_plant:*

```
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
```

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				5
No.	Score	Match	Length	 DB	ID	Description
1	1817.5	85.0	390	6	Q9TUM8	Q9tum8 equus cabal
2	1738.5	81.3	368	11	Q8R4D9	Q8r4d9 sigmodon hi
3	854.5	39.9	379	13	Q8JHF5	Q8jhf5 sparus aura
4	850.5	39.8	379	13	Q8AXK8	Q8axk8 sparus aura
5	832.5	38.9	412	11	Q91YU7	Q91yu7 mus musculu
6	832	38.9	382	13	Q9PWA9	Q9pwa9 morone chry
7	826	38.6	414	11	Q91VP5	Q91vp5 mus musculu
8	810	37.9	382	13	093449	093449 oncorhynchu
9	780	36.5	376	13	Q9PTQ2	Q9ptq2 cyprinus ca
10	765	35.8	399	11	Q9ERB7	Q9erb7 mesocricetu
11	724.5	33.9	362	11	Q99K17	Q99k17 mus musculu
12	693.5	32.4	130	11	Q08714	Q08714 mesocricetu
13	678.5	31.7	361	13	Q98854	Q98854 cyprinus ca
14	676.5	31.6	124	6	Q95N80	Q95n80 canis famil
15	638	29.8	112	6	002730	002730 oryctolagus
16	605	28.3	255	11	Q921T1	Q921t1 mus musculu
17	586.5	27.4	127	6	Q9TV08	Q9tv08 canis famil
18	575	26.9	224	11	Q8CDZ9	Q8cdz9 mus musculu
19	563.5	26.3	200	13	Q90YF1	Q90yf1 pleuronecte
20	554	25.9	101	11	Q9R184	Q9r184 meriones un
21	461	21.6	179	13	Q90YF2	Q90yf2 pleuronecte
22	413	19.3	88	13	Q90YF5	Q90yf5 pleuronecte
23	402	18.8	88	13	Q90YF7	Q90yf7 oncorhynchu
24	397	18.6	88	13	Q90ZE7	Q90ze7 acipenser b
25	393	18.4	87	13	042306	042306 carassius a
26	383	17.9	91	6	Q9MYZ1	Q9myz1 capra hircu
27	376.5	17.6	309	4	Q8WV88	Q8wv88 homo sapien
28	373	17.4	86	6	Q28241	Q28241 cervus elap
29	358	16.7	81	6	Q9N1S3	Q9n1s3 capreolus c
30	340.5	15.9	375	13	8DWD8	Q8uwd8 columba liv
31	327.5	15.3	375	13	Q8AVB2	Q8avb2 coturnix co
32	325.5	15.2	375	13	Q8UWD7	Q8uwd7 coturnix ch
33 34	325.5	15.2	389	13	Q90YY0	Q90yy0 ictalurus p
34 35	320.5 320	15.0 15.0	375	13	Q98SP0	Q98sp0 gallus gall
36			87	13	Q8JHB6	Q8jhb6 scophthalmu
36	317.5 317.5	14.8	375	6	Q9GM97	Q9gm97 equus cabal Q8uwe0 anas platyr
38	317.5	14.8 14.8	375 77	13 13	Q8UWE0 Q90YF8	Q90yf8 oncorhynchu
39	315.5	14.7	375	13	Q8UWD9	Q8uwd9 anser anser
40	313.5	14.7	375	6	Q80WD9 Q8HY52	Q8hy52 lepus capen
40	313.3	14./	213	O	QORIDZ	Zonyoz repus capen

```
Q95j86 macaca fasc
    310.5 14.5 375 6 Q95J86
41
                                                    028240 cervus elap
42
     302 14.1
                   50 6 Q28240
                    62 13 090ZJ7
                                                     090zj7 anguilla an
43
      301 14.1
           14.1 376 13 Q98TB4
14.0 375 6 Q8WNS6
                   376 13 Q98TB4
      301 14.1
                                                     098tb4 oreochromis
44
                                                    Q8wns6 bos taurus
45
    300.5
```

ALIGNMENTS

```
RESULT 1
Q9TUM8
ΙD
    Q9TUM8
                PRELIMINARY; PRT;
                                        390 AA.
AC
    Q9TUM8;
    01-MAY-2000 (TrEMBLrel. 13, Created)
DT
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
    Transforming growth factor beta 1.
DE
    TGFB1.
GN
OS
    Equus caballus (Horse).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC
OX
    NCBI TaxID=9796;
RN
    [1]
RP
    SEQUENCE FROM N.A.
    Nixon A.J., Brower-Toland B.T., Sandell L.J.;
RA
RT
    "Molecular cloning of equine transforming growth factor beta 1 reveals
    a divergent nucleotide structure that encodes a novel bioactive
RT
    peptide among mammalian species.";
RT
    Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RL
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
    EMBL; AF175709; AAD49431.1; -.
DR
    HSSP; P01137; 1KLA.
DR
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    InterPro; IPR003911; TGF TGFb.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
SO
    SEQUENCE 390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;
 Query Match 85.0%; Score 1817.5; DB 6; Length 390; Best Local Similarity 86.4%; Pred. No. 1e-152;
 Matches 348; Conservative 12; Mismatches 30; Indels 13; Gaps
                                                                          1;
           1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
Oy
             Db
           1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLA 60
          61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
Qу
             61 SPPSQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEI 120
Db
```

```
121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
QУ
                    121 YKTVETGSHSIYMFFNASELRAAVPDPMLLSRAELRLLRLKLSVEQHVELYQKYSNNSWR 180
Db
         181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qу
             Db
         181 YLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGLRLSAHCPCDSKDNTLRVGINGFS 240
         241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFS 300
Qу
             1111111
         241 SSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRHRR--
                                                        ---ALDTNYCSS 287
Dh
         301 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 360
Qу
             288 STEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHN 347
Db
         361 PGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
             348 PGASAAPCCVPOVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
Db
RESULT 2
Q8R4D9
ID
    Q8R4D9
               PRELIMINARY;
                               PRT; 368 AA.
AC
    Q8R4D9;
    01-JUN-2002 (TrEMBLrel. 21, Created)
DT
    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DТ
    Transforming growth factor beta-1 protein (Fragment).
DE
GN
    Sigmodon hispidus (Hispid cotton rat).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC
OC
    Sigmodon.
OX
    NCBI TaxID=42415;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Blanco J.C., Pletneva L.M., Prince G.A.;
    "Cotton rat cytokines, chemokines, and interferons.";
RT
RL
    Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF480858; AAL87199.1; -.
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
FT
    NON TER
                 1
SO
    SEOUENCE
              368 AA; 41905 MW; A5C91207B0468B4A CRC64;
 Query Match 81.3%; Score 1738.5; DB 11; Length 368; Best Local Similarity 85.3%; Pred. No. 9.8e-146;
```

```
Matches 325; Conservative 16; Mismatches 27; Indels
                                                      13; Gaps
                                                                  1;
         23 PGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYN 82
Qу
            Db
          1 PGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYN 60
Qу
         83 STRDRVAGESVEPEPEADYYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLFNTSELRE 142
            61 STRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAIYDKTKDIPHSVYMFFNTSDIRE 120
Dh
        143 AVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTG 202
Qу
            121 AVPEPPLLSRAELRLQRFKSNVEQHVELYEKYSNNSWRYLGNRLLSPTDSPEWLSFDVTS 180
Db
        203 VVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMA 262
QУ
            181 VVRKWLNGGDGIOGFRFSAHCSCDSKDNILHVEINGISPKRRGDLGTIHDMNRPFLLLMA 240
Db
        263 TPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWK 322
QУ
            241 TPLERAOHLHSSRHRR------ALDTNYCFSSTEKNCCVROLYIDFRKDLGWK 287
Db
        323 WIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYY 382
QУ
            Db
        288 WIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPQALEPLPIVYY 347
        383 VGRKPKVEQLSNMIVRSCKCS 403
Qу
            1111111111111111111
Db
        348 VGRKPKVEQLSNMIVRSCKCS 368
RESULT 3
Q8JHF5
ΙĐ
    Q8JHF5
              PRELIMINARY;
                              PRT;
                                   379 AA.
AC
    08JHF5:
DT
    01-OCT-2002 (TrEMBLrel. 22, Created)
DT
    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
    Transforming growth factor beta 1.
OS
    Sparus aurata (Gilthead sea bream).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
OC
    Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC
    Sparidae; Sparus.
OX
    NCBI TaxID=8175;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
    Tafalla C., Aranguren R., Secombes C.J., Castrillo J.L., Novoa B.,
RA
RA
    Figueras A.;
RT
    "Molecular characterization of sea bream (Sparus aurata) transforming
RT
    growth factor beta1.";
RL
    Fish and Shellfish Immunol. 0:0-0(2002).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; AF510084; AAN03842.1; -.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb N.
```

```
DR
        InterPro; IPR003911; TGF TGFb.
DR
        Pfam; PF00019; TGF-beta; 1.
DR
        Pfam; PF00688; TGFb propeptide; 2.
        PRINTS; PR00438; GFCYSKNOT.
DR
        PRINTS; PR01423; TGFBETA.
DR
        ProDom; PD000357; TGFb; 1.
DR
DR
        SMART; SM00204; TGFB; 1.
DR
        PROSITE; PS00250; TGF_BETA_1; 1.
        SEQUENCE 379 AA; 43506 MW; C0C9D3D2FCA29C0E CRC64;
SQ
                                             39.9%; Score 854.5; DB 13; Length 379;
   Query Match
   Best Local Similarity 46.2%; Pred. No. 2.7e-67;
   Matches 187; Conservative 69; Mismatches 108; Indels 41; Gaps
                                                                                                                                     15:
                   12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL-ASPPSQGDVPP 70
Qу
                         3 LVFLMFMVAYTVGK-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPTESPQAGD--E 59
Db
                   71 GPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNOIYDKFK 125
Qу
                            :| ::|:|||||:: : : | :
                                                                          : [ : [ : ] |
                   60 EEIPSSLLSLYNSTKEMLKEQQTEVQTDIFTEQEEEEYFA---TRVHKFNTTNPV----- 111
Db
                 126 GTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV---EQHVELYQKYSNDSWRYL 182
Qу
                           Db
                 112 RTPQNMSMSFNISEIRRSIGDYRLLTTAELRML-IKAPTILDEQRVELYQGLGT-SPRYL 169
                 183 SNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTLHVEINGFN 240
Qу
                                            :: | :
                 170 ASRFITNELRDKWLSFDVTETLONWLKGNDDVQVFQLRLYCDCGRSSDVSTFSFGISGMT 229
Db
                 241 SGRRGDLATIHGMNR--PFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYC 298
Qу
                         : | | | | | : | : | : | | : | : | | : | | : | | : | | | : | | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | : | : | | | : | : | | | : | : | | | : | : | | : | | : | : | | : | | : | : | | | : | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                 230 AG-RGDKAVLDDMTKQPPYILTMSIPKNVSSHL-TSRKKRSTETKD------TC 275
Db
                 299 FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQ 358
Qу
                          276 TAQTE-TCCVRSLYIDFRKDLGWKWIHKPTRYHANYCMGSCTYIWNAENKYSQILALYKH 334
Db
                 359 HNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
                         Db
                 335 HNPGASAQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 379
RESULT 4
Q8AXK8
                              PRELIMINARY;
                                                             PRT;
                                                                         379 AA.
ΙD
        Q8AXK8
AC
        Q8AXK8;
DT
         01-MAR-2003 (TrEMBLrel. 23, Created)
        01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT
        01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
        Transforming growth factor beta 1.
DE
OS
        Sparus aurata (Gilthead sea bream).
OC
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
OC
        Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC
        Sparidae; Sparus.
        NCBI TaxID=8175;
OX
```

```
RN
    [1]
RP
    SEQUENCE FROM N.A.
    Tafalla C., Novoa B., Aranguren R., Figueras A.;
RA
    "Molecular cloning and characterization of sea bream (Sparus aurata)
RT
    TGF beta 1.":
RT
    Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RL
    EMBL; AF424703; AAN76665.1; -.
DR
    SEQUENCE 379 AA; 43485 MW; A306EC387F6DBA7C CRC64;
SO
                      39.8%; Score 850.5; DB 13; Length 379;
 Query Match
 Best Local Similarity 46.2%; Pred. No. 6e-67;
 Matches 187; Conservative 68; Mismatches 109; Indels
         12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL-ASPPSQGDVPP 70
Qу
            Db
          3 LVFLMFMVAYTVGK-VSGMSTCKTLDLEMVKKKRIEAIRSOILSKLRLPTESPQAGD--E 59
         71 GPLPEAVLALYNSTRDRVAGESVEPEPE----PEADYYAKEVTRVLMVESGNQIYDKFK 125
Qу
              :|::|:|||||
         60 EEIPSSLLSLYNSTKEMLKEOOTEVOTDIFTEXEEEEYFA---TRVHKFNTTNPV----- 111
Db
        126 GTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV---EQHVELYQKYSNDSWRYL 182
Qу
             112 RTPONMSMSFNISEIRRSIGDYRLLTTAELRML-IKAPTILDEORVELYOGLGT-SPRYL 169
Db
        183 SNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGF--RLSAHSSSDSKDNTLHVEINGFN 240
Qу
                      :|||||| :: || ::: | ||
                                                 | : |
        170 ASRFITNELRDKWLSFDVTETLQNWLKGNDDVQVFQLRLYCDCGRSSDVSTFSFGISGMT 229
Db
        241 SGRRGDLATIHGMNR--PFLLLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYC 298
Qу
            230 AG-RGDKAVLDDMTKQPPYILTMSIPKNVSSHL-TSRKKRSTETKD-----TC 275
Db
        299 FSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQ 358
Qу
             276 TAQTE-TCCVRSLYIDFRKDLGWKWIHKPTRYHANYCMGSCTYIWNAENKYSQXLALYKH 334
Db
         359 HNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            Db
         335 HNPGASAQPCCVPOALEPLPILYYVGROHKVEOLSNMIVKSCKCS 379
RESULT 5
091YU7
ΙD
    O91YU7
              PRELIMINARY;
                              PRT;
                                    412 AA.
AC
    O91YU7;
DT
    01-DEC-2001 (TrEMBLrel. 19, Created)
DT
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
    Transforming growth factor, beta 3.
DE
GN
    TGFB3.
    Mus musculus (Mouse).
OS
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
    NCBI TaxID=10090;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
```

```
RA
    Strausberg R.;
RL
    Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
    EMBL; BC014690; AAH14690.1; -.
DR
    MGD; MGI:98727; Tgfb3.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
DR
    PROSITE; PS00250; TGF BETA 1; 1.
    SEQUENCE 412 AA; 47144 MW; F3EB65D046DF32AD CRC64;
SO
                     38.9%; Score 832.5; DB 11; Length 412;
 Ouery Match
 Best Local Similarity 44.7%; Pred. No. 2.7e-65;
 Matches 188; Conservative 58; Mismatches 126; Indels
                                                      49; Gaps
                                                                13;
         15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
Qу
                   1: 1:1
          9 LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP 66
Db
         75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNOIYDKFKG 126
Qу
             67 YOVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 126
Db
        127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEOHVELYQKYSND----S 178
Qу
                               :: || | : :
        127 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 182
Db
        179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Qу
             : | :|
        183 ORYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV 242
Db
        231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
QУ
              243 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRK---- 298
Db
        283 NDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYI 342
Qу
                  Db
        299 -----KRALDTNYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYL 351
        343 WSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC 402
Qу
             352 RSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKC 411
Db
        403 S 403
Qу
        412 S 412
Dh
```

```
ID
     O9PWA9
                 PRELIMINARY;
                                    PRT;
                                           382 AA.
AC
     09PWA9:
DT
     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE
     Transforming growth factor beta precursor.
GN
     TGF-BETA.
OS
     Morone chrysops x Morone saxatilis (white bass x striped bass).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
     Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
     Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC
     Moronidae; Morone.
OX
     NCBI TaxID=45352;
RN
     [1]
RP
     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC
     TISSUE=KIDNEY;
RX
     MEDLINE=20394636; PubMed=10938723;
     Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
RA
     Tompkins W.A.F.;
RA
     "Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
RT
RT
     chrysops) transforming growth factor-beta (TGF-beta), and development
     of a reverse transcription quantitative competitive polymerase chain
RT
RT
     reaction (RT-qcPCR) assay to measure TGF-beta mRNA of teleost fish.";
RL
     Fish Shellfish Immunol. 10:61-85(2000).
     -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
CC
         RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
CC
     -!- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONUCLEAR CELLS FROM
CC
         PERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.
CC
     -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
     EMBL; AF140363; AAD46997.1; -.
     HSSP; P01137; 1KLA.
DR
DR
     InterPro; IPR002400; GF cysknot.
     InterPro; IPR001839; TGFb.
DR
     InterPro; IPR001111; TGFb_N.
DR
     InterPro; IPR003911; TGF TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
DR
     Pfam; PF00688; TGFb_propeptide; 1.
DR
     PRINTS; PR00438; GFCYSKNOT.
DR
DR
     PRINTS; PR01423; TGFBETA.
     ProDom: PD000357; TGFb; 1.
DR
     SMART; SM00204; TGFB; 1.
DR
     PROSITE; PS00250; TGF BETA 1; 1.
DR
KW
     Growth factor; Mitogen; Glycoprotein; Signal.
FT
     SIGNAL
                   1
                          ?
                                   POTENTIAL.
FT
     PROPEP
                   ?
                         270
FT
                        382
                                   TRANSFORMING GROWTH FACTOR BETA.
     CHAIN
                 271
                 278
                        286
FT
     DISULFID
                                   BY SIMILARITY.
FT
     DISULFID
                 285
                        348
                                   BY SIMILARITY.
FT
     DISULFID
                 314
                        379
                                   BY SIMILARITY.
FT
     DISULFID
                 318
                        381
                                   BY SIMILARITY.
                                   INTERCHAIN (BY SIMILARITY).
FT
     DISULFID
                 347
                        347
                  73
                         73
FT
     CARBOHYD
                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
     CARBOHYD
                 108
                       108
                                  N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
                        113
                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
     CARBOHYD
                 113
FT
     CARBOHYD
                 124
                        124
                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
     CARBOHYD
                 259
                        259
                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
```

```
235 237 CELL ATTACHMENT SITE (POTENTIAL).
FT
        SITE
                            382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;
SO
        SEOUENCE
                                              38.9%; Score 832; DB 13; Length 382;
   Query Match
   Best Local Similarity 45.9%; Pred. No. 2.7e-65;
   Matches 187; Conservative 64; Mismatches 108; Indels
                                                                                                                  48; Gaps
                                                                                                                                        15:
                   15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL---ASPPSQGDVPPG 71
Qу
                         6 LMLVVVYTVGN-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLPKEPEPDQAGDEEEI 64
Db
                   72 PLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDKFKG 126
Qу
                         65 PTP--LLSLYNSTKEMLKEQQTEVQTDISTEQEEEEYFAKVLHKFNMTRKNN------ 114
Db
                  127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV--EQHVELYQKYSNDSWRYLSN 184
Qу
                         115 TDTTKKMFFNISEIRESVGDYRLLTSAELRMLIKKTTIYDEQRVELYSGL-GDSPRYLAS 173
Db
                  185 RLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTL-HVEINGFNS 241
Qу
                                         : [ ] [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [ : ] : [
                  174 RFITNKWKDKWLSFDVTKTLQDWLKGTDDEQGFQLRLFCECNKVSAGETIFKFGISGIDP 233
Db
                  242 GRRGDLATIHGMNR--PFLLLMATPLERAQHLHS---SRHRRALDTNDYKDDDDKALDTN 296
QУ
                                      234 G-RGDTGPMOLLTOOPPYILTMSIP----QNISSPSTSRKKRSTETKD----- 276
Db
                  297 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 356
QУ
                           277 VCTAQTE-TCCVRSLYIDFRKDLGWKWIHKPTGYNANYCMGSCTYIWNAENKYSQILALY 335
Db
                  357 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
                             336 KHHNPGASAQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS 382
Db
RESULT 7
Q91VP5
ID
         Q91VP5
                              PRELIMINARY;
                                                           PRT:
                                                                           414 AA.
AC
         Q91VP5;
         01-DEC-2001 (TrEMBLrel. 19, Created)
DT
         01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DT
DE
         Similar to transforming growth factor, beta 2.
         TGFB2.
GN
OS
         Mus musculus (Mouse).
OC
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
         NCBI TaxID=10090;
RN
         [1]
         SEQUENCE FROM N.A.
RP
RC
         TISSUE=Breast tumor;
RA
         Strausberg R.;
RL
         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
         -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
DR
         EMBL; BC011170; AAH11170.1; -.
         MGD; MGI:98726; Tgfb2.
DR
```

```
InterPro; IPR002400; GF cysknot.
DR
DR
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
    ProDom; PD000357; TGFb; 1.
DR
DR
    SMART; SM00204; TGFB; 1.
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    SEQUENCE 414 AA; 47588 MW; DB37A7C38881F286 CRC64;
SQ
 Query Match
                      38.6%; Score 826; DB 11; Length 414;
 Best Local Similarity 43.7%; Pred. No. 1e-64;
 Matches 188; Conservative 63; Mismatches 121; Indels 58; Gaps
                                                                15;
         12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVP-P 70
Qу
                5 VLSTFLLLHLVP--VALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEP 60
Db
         71 GPLPEAVLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYD 122
Qу
             61 DEVPPEVISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHLPSENAIPP 120
Db
        123 KFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----K 173
Qу
                                  121 TFY-RPYFRIVRFDVSTMEKNASN---LVKAEFRVFRLQNPKARVAEQRIELYQILKSKD 176
Db
        174 YSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSS----- 225
Qу
                             :: : ||: ::::
        177 LTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVQEWLHHKDRNLGFKISLHCPCCTFVPSNN 236
Db
        226 ---DSKDNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHS 273
Qу
                         237 YIIPNKSEELEARFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHLLLMLLPSYRLESQQS 296
Db
        274 SRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHAN 333
Qу
                          | | ::
        297 SRRKK-----RALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNAN 344
Db
        334 FCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS 393
Qу
            345 FCAGACPYLWSSDTOHTKVLSLYNTINPEASASPCCVSQDLEPLTILYYIGNTPKIEQLS 404
Db
        394 NMIVRSCKCS 403
Qу
            405 NMIVKSCKCS 414
Db
RESULT 8
093449
              PRELIMINARY;
                             PRT;
                                   382 AA.
    093449
ID
    093449; Q91217;
AC
    01-NOV-1998 (TrEMBLrel. 08, Created)
DT
    01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
```

```
DE
     Transforming growth factor beta precursor.
GN
     TGF-BETA OR TGF.
     Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC
     Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC
OX
     NCBI TaxID=8022;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RC
     TISSUE=LEUKOCYTE;
RX
     MEDLINE=99242020; PubMed=10227481;
RA
     Daniels G.D., Secombes C.J.;
     "Genomic organisation of rainbow trout, Oncorhynchus mykiss TGF-
RT
RT
     BETA.";
RL
     Dev. Comp. Immunol. 23:139-147(1999).
RN
     [2]
RP
     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC
     TISSUE=LEUKOCYTE;
     MEDLINE=98390168; PubMed=9722928;
RX
     Hardie L.J., Laing K.J., Daniels G.D., Grabowski P.S., Cunningham C.,
RA
RA
     Secombes C.J.;
RT
     "Isolation of the first piscine transforming growth factor beta gene:
     analysis reveals tissue specific expression and a potential regulatory
RT
RT
     sequence in rainbow trout (Oncorhynchus mykiss).";
RL
     Cytokine 10:555-563(1998).
     -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
CC
         RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
CC
     -!- TISSUE SPECIFICITY: EXPRESSED IN BLOOD LEUKOCYTES, KIDNEY
         MACROPHAGES, BRAIN, GILL AND SPLEEN BUT NOT IN LIVER.
CC
     -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
     EMBL; AJ007836; CAA07707.1; -.
DR
     EMBL; X99303; CAA67685.1; -.
DR
DR
     HSSP; P01137; 1KLA.
     InterPro; IPR002400; GF cysknot.
DR
     InterPro; IPR001839; TGFb.
DR
     InterPro; IPR001111; TGFb N.
DR
DR
     InterPro; IPR003911; TGF TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
DR
     Pfam; PF00688; TGFb propeptide; 1.
DR
     PRINTS; PR00438; GFCYSKNOT.
     PRINTS; PR01423; TGFBETA.
DR
     ProDom; PD000357; TGFb; 1.
DR
DR
     SMART; SM00204; TGFB; 1.
     PROSITE; PS00250; TGF_BETA_1; 1.
DR
KW
     Growth factor; Mitogen; Glycoprotein; Signal.
FΤ
     SIGNAL
                   1
                         20
                                   POTENTIAL.
FT
     PROPEP
                  21
                        270
FT
     CHAIN
                 271
                         382
                                   TRANSFORMING GROWTH FACTOR BETA.
FT
                        286
     DISULFID
                 278
                                   BY SIMILARITY.
FT
     DISULFID
                 285
                        348
                                   BY SIMILARITY.
FT
     DISULFID
                 314
                        379
                                   BY SIMILARITY.
FT
     DISULFID
                 318
                        381
                                  BY SIMILARITY.
     DISULFID
                        347
FT
                 347
                                   INTERCHAIN (BY SIMILARITY).
                 76
                        76
FT
     CARBOHYD
                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
     CARBOHYD
                 116
                        116
                                   N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT
FT
     CARBOHYD
                 125
                        125
                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
237
                     237
                             N \rightarrow D (IN REF. 2).
FΤ
    CONFLICT
                             Q -> H (IN REF. 2).
FT
               345
                     345
    CONFLICT
                             LS -> VP (IN REF. 2).
FT
    CONFLICT
              371
                     372
                     377
                             K \rightarrow M (IN REF. 2).
FT
    CONFLICT
              377
    SEQUENCE 382 AA; 44136 MW; 93BD4D3540084B92 CRC64;
SQ
                      37.9%; Score 810; DB 13; Length 382;
 Query Match
 Best Local Similarity 46.8%; Pred. No. 2.4e-63;
 Matches 182; Conservative 58; Mismatches 105; Indels 44; Gaps
                                                                   14:
         30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPP---SQGDVPPGPLPEAVLALYNSTRD 86
Qу
            -:|:::::||||:
         23 MSTCKSLDLELVKRKRIEAIRGQILSKLRLPKEPEIDQEGDTE--EVPASLMSIYNSTVE 80
Db
         87 RVAGESVE-----PEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSEL 140
Qу
                         : | || |:|| || : | : | |
                                                 : | : ||| ||:
         81 -LSEEQVHTYIPSTQDAEEEA-YFAKEVHKFNMKQSENT-----SKHQI--LFNMSEM 129
Db
        141 REAVPEPVLLSRAELRLL----RLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWL 196
Qу
                              1
                                    130 RSVLGTDRLLSQAELRLLIKNHGLLDDSEQRLELYRGV-GDKARYLKSHFVSKEWANRWV 188
Db
        197 SFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATI--HGMN 254
Qу
                                              : | : | _ [ _
            ||: |:
        189 SFDVTOTLNEWLOGAGEEOGFOLKLPCDCGKPMEEFRFKISGMNK-LRGNTETLAMKMPS 247
Db
        255 RPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYID 314
Qy
            248 KPHILLMSLPVERHSOL-SSRKKROTTTEE-----IC-SDKSESCCVRKLYID 293
Db
        315 FRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQAL 374
Qу
            294 FRKDLGWKWIHEPTGYFANYCIGPCTYIWNTENKYSQVLALYKHNPGASAQPCCVPQVL 353
Db
        375 EPLPIVYYVGRKPKVEQLSNMIVRSCKCS 403
Qу
            354 EPLPIIYYVGRQHKVEQLSNMIVKSCRCS 382
Db
RESULT 9
Q9PTQ2
                               PRT;
                                     376 AA.
ΙD
    Q9PTQ2
               PRELIMINARY;
AC
    Q9PTQ2;
    01-MAY-2000 (TrEMBLrel. 13, Created)
DT
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DE
    Transforming growth factor beta precursor.
OS
    Cyprinus carpio (Common carp).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC
OC
    Cyprinidae; Cyprinus.
OX
    NCBI_TaxID=7962;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RA
    Yin Z., Kuang J.;
RT
    "Molecular cloning of carp transforming growth factor beta 1.";
    Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RI.
```

```
-!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC
        RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
    EMBL; AF136947; AAF22573.1; -.
DR
    HSSP; P01137; 1KLA.
DR
DR
    InterPro; IPR001839; TGFb.
    InterPro; IPR001111; TGFb_N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
    Growth factor; Mitogen; Glycoprotein; Signal.
KW
    SIGNAL
                     22
                              POTENTIAL.
FT
                1
    PROPEP
               23
                     264
FT
                              TRANSFORMING GROWTH FACTOR BETA.
FT
    CHAIN
               265
                     376
                              BY SIMILARITY.
FT
    DISULFID
               272
                     280
                              BY SIMILARITY.
FT
    DISULFID
               308
                     373
                     375
                              BY SIMILARITY.
FT
    DISULFID
              312
                    341
FT
    DISULFID 341
                              INTERCHAIN (BY SIMILARITY).
                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
                     76
FT
    CARBOHYD
              76
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD 125
                    125
    CARBOHYD
                              N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
             167
                    167
                            CELL ATTACHMENT SITE (POTENTIAL).
FT
    SITE
              230
                     232
    SEQUENCE
              376 AA; 43329 MW; 7F7FC4DA58B69681 CRC64;
SO
                      36.5%; Score 780; DB 13; Length 376;
 Query Match
 Best Local Similarity 44.0%; Pred. No. 1.1e-60;
 Matches 179; Conservative 65; Mismatches 121; Indels
                                                        42; Gaps
                                                                   15;
          6 LRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQ 65
Qу
            Db
          1 MRVESLLLALQCLLGFV--HYSGALSTCSPLDLELIKRKRIEAIRGQILSKLRLSKEPEV 58
         66 GDVPPGP-LPEAVLALYNST---RDRVAGESVEPEPEP-EADYYAKEVTR--VLMVESGN 118
Qу
                   59 DEEKESONIPAELISVYNSTVELNEEQAAPPEOPKEDPVEEEYYAKEVHKFTIKLMEKNP 118
Db
         119 QIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLK--VEQHVELYQKYSN 176
Qу
                  : || ::: : : ::|: || || ||
                                                      119 ---DKF-----LWFNITDISQTLGLNRIISQVELRLLITTFPDGSEQRLELYQVIGN 167
Dh
         177 DSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEI 236
Qу
             Db
         168 KS-RYLESRFI--PNQRKWLSFDVTQTLKDWLQRSEAEQGFQLKMADNCDPQ-KTFQLKI 223
         237 NGFNSGRRGDLATIH-GMNRPFLLLMATPLERAQHLHSSRHRRALDTNDYKDDDDKALDT 295
Qу
                  224 PGLVL-VRGDTETLAVNMPRPHILVMSLPLDGN---NSSKSRRKRQT-----ET 268
Db
         296 NYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAL 355
Qу
                     269 DQVCTDKSDGCCVRSLYIDFRKDLGWKWIHEPSGYYANYCTGSCSFVWTSENKYSOVLAL 328
Dh
```

```
Qу
         356 YNOHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKC 402
               329 YKHHNPGASAQPCRVPQVLNPLPIFYYVGRQHKVEQLSNMIVKTCKC 375
Db
RESULT 10
Q9ERB7
ID
    Q9ERB7
               PRELIMINARY;
                               PRT; 399 AA.
AC
    O9ERB7;
DT
    01-MAR-2001 (TrEMBLrel. 16, Created)
DT
    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT
    01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE
    Transforming growth factor-beta 2 (Fragment).
    Mesocricetus auratus (Golden hamster).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC
OC
    Mesocricetus.
    NCBI_TaxID=10036;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
    Ramesh G., Kondaiah P., Seshagiri P.B.;
RA
    "Differential expression and selective localization of transforming
RT
    growth factor-beta isoforms in the hamster uterus during estrous
RT
RT
    cycle.";
    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RL
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
    EMBL; AY007214; AAG02247.1; -.
DR
    HSSP; P08112; 2TGI.
DR
    InterPro; IPR001839; TGFb.
DR
DR
    InterPro; IPR001111; TGFb_N.
DR
    InterPro; IPR003911; TGF_TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
    Pfam; PF00688; TGFb propeptide; 1.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
FT
    NON TER
                1
FT
    NON TER
               399
                     399
    SEQUENCE
              399 AA; 46078 MW; A6FF8E65EAFD5148 CRC64;
SQ
                        35.8%; Score 765; DB 11; Length 399;
 Ouery Match
 Best Local Similarity 42.5%; Pred. No. 2.5e-59;
 Matches 177; Conservative 60; Mismatches 121; Indels 58; Gaps
          18 LLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGOILSKLRLASPPSOGDVP-PGPLPEA 76
Qу
             4 LLHLVP--VALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEPDEVPPE 59
Db
          77 VLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYDKFKGTP 128
Qу
                       1:::|||||
                                                      60 VISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHFPSENAIPPTFY-RP 118
Db
         129 HSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----KYSNDSW 179
Qу
                               : : |: | : :
Db
         119 YFRIVRFDVSMMEKNASN---LVKAEFRVFRLQNPKARVAEQRIELYQILKSKDLTSPTQ 175
```

```
180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH------SSSDSK 228
Qу
                                                         : :
             | | : ::::
                         176 RYIDSKVVKTRAEGEWLSFDVTDAVHEWLHHKDRNLGFKISLHCPCCTFVPFNNNIIPNK 235
Db
         229 DNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAOHLHSSRHRRA 279
Qу
                    236 SEELEARFAGIDGTSQHSSGHQETIKSTRKKNSGKTPHLLLMLLPSYRLESQQSNRRKK- 294
Db
         280 LDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPC 339
Qу
                       295 -----RALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGAC 343
Db
         340 PYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNM 395
Qу
             ]|:|| |||::|||:|||:||
         344 PYLWSSDTQHTKVLSLYNTINPEASASPCCVSHDLEPLTILYYIGNTPKIEQLSNM 399
Db
RESULT 11
099K17
               PRELIMINARY;
                                PRT;
                                      362 AA.
ID
    Q99K17
AC
    Q99K17;
    01-JUN-2001 (TrEMBLrel. 17, Created)
DT
    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DТ
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DТ
DE
    Similar to transforming growth factor, beta 3 (Fragment).
GN
    TGFB3.
OS
    Mus musculus (Mouse).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RA
    Strausberg R.;
    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RL
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
    EMBL; BC005513; AAH05513.1; -.
DR
DR
    HSSP; P10600; 1TGJ.
    MGD; MGI:98727; Tgfb3.
DR
    InterPro; IPR002400; GF cysknot.
DR
    InterPro: IPR001839: TGFb.
DR
DR
    InterPro; IPR001111; TGFb N.
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 1.
DR
    PRINTS; PR00438; GFCYSKNOT.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF_BETA_1; 1.
DR
    NON TER
FΤ
                 1
SQ
    SEQUENCE
              362 AA; 41486 MW; 0808E46180FDAE70 CRC64;
                       33.9%; Score 724.5; DB 11; Length 362;
 Query Match
 Best Local Similarity 43.4%; Pred. No. 8.5e-56;
 Matches 164; Conservative 52; Mismatches 113; Indels
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58 RLASPPSQGDVPPGPLPEAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVL 112

Qу

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Db
          2 RVGSPPEPSVMT--HVPYQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFD 59
        113 MVE---SGNOIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVE 165
Qу
                             :: || | : :
                                               ::
                         11
         60 MIQGLAEHNELAVCPKGITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTE 115
Db
         166 OHVELYOKYSND----SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSA 221
Qу
                            116 QRIELFQILRPDEHIAKORYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISI 175
Db
         222 H-----SSSDSKDN---TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPL 265
Qу
                    176 HCPCHTFQPNGDILENVHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPP 235
Db
         266 ERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIH 325
Qу
                      |:
                                  236 HRLDSPGQGSQRK-----KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVH 284
Db
         326 EPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGR 385
QУ
            285 EPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGR 344
Db
         386 KPKVEOLSNMIVRSCKCS 403
Qу
             1111111111
Db
         345 TPKVEQLSNMVVKSCKCS 362
RESULT 12
008714
ID
    008714
               PRELIMINARY;
                               PRT;
                                     130 AA.
    Q08714; 070331;
AC
    01-NOV-1996 (TrEMBLrel. 01, Created)
DT
    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
    Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
DE
GN
    TGFB1.
    Mesocricetus auratus (Golden hamster).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
\mathsf{OC}
OC
    Mesocricetus.
    NCBI TaxID=10036;
OX
RN
    [1]
    SEQUENCE FROM N.A.
RP
RC
    STRAIN=LVG (SYR);
RX
    MEDLINE=93304479; PubMed=8317544;
    Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
RA
RA
    Elovic A., McBride J., Gallagher G., Todd R.;
    "Sequential expression of transforming growth factors alpha and beta 1
RT
RT
    by eosinophils during cutaneous wound healing in the hamster.";
    Am. J. Pathol. 143:130-142(1993).
RL
RN
    [2]
    SEQUENCE OF 26-115 FROM N.A.
RP
RC
    STRAIN=SYRIAN; TISSUE=SPLEEN;
    MEDLINE=98234044; PubMed=9573100;
RX
    Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RA
RT
    "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
```

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analysis of cytokine mRNA expression in experimental visceral
RT
RT
    leishmaniasis.";
    Infect. Immun. 66:2135-2142(1998).
RL
     -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC
        PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
        TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC
        THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC
        REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC
CC
        DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC
     -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
CC
DR
    EMBL; X60296; CAA42838.1; -.
DR
    EMBL; AF046214; AAC40099.1; -.
    HSSP; P01137; 1KLA.
DR
DR
     InterPro; IPR001839; TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
DR
    ProDom; PD000357; TGFb; 1.
DR
     SMART; SM00204; TGFB; 1.
DR
     PROSITE; PS00250; TGF BETA 1; 1.
KW
    Growth factor; Mitogen; Glycoprotein.
FT
    NON TER
                  1
                         1
FT
     PROPEP
                        18
                 <1
                                 TRANSFORMING GROWTH FACTOR BETA 1.
FT
    CHAIN
                 19
                       130
FT
    DISULFID
                 25
                        34
                                BY SIMILARITY.
FT
    DISULFID
                 33
                        96
                                BY SIMILARITY.
                       129
                                BY SIMILARITY.
FT
    DISULFID
                 66
                 95
                        95
                                 INTERCHAIN (BY SIMILARITY).
FT
    DISULFID
FΤ
     CONFLICT
                 93
                        93
                                G \rightarrow S (IN REF. 2).
               130 AA; 14997 MW; 8B41DD6CF39CCA77 CRC64;
SQ
    SEQUENCE
                         32.4%; Score 693.5; DB 11; Length 130;
  Query Match
  Best Local Similarity 88.8%; Pred. No. 1.1e-53;
  Matches 127; Conservative 0; Mismatches 3; Indels
                                                             13; Gaps
                                                                          1;
         261 MATPLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLG 320
Qу
              1 MATPLERAQHLQSSRHRR------ALDTNYCFSSTEKNCCVRQLYIDFRKDLG 47
Db
         321 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIV 380
Qу
              48 WKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAGPCCVPQALEPLPIV 107
Db
         381 YYVGRKPKVEQLSNMIVRSCKCS 403
Qу
              Db
          108 YYVGRKPKVEQLSNMIVRSYKCS 130
RESULT 13
098854
ID
     Q98854
                PRELIMINARY;
                                  PRT:
                                        361 AA.
AC
     Q98854;
DT
     01-FEB-1997 (TrEMBLrel. 02, Created)
     01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DТ
     01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DТ
     Transforming growth factor beta 2 (TGF-beta 2) (Fragment).
DE
GN
     TGFB2.
OS
     Cyprinus carpio (Common carp).
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC
    Cyprinidae; Cyprinus.
OX
    NCBI TaxID=7962;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RC
    TISSUE=HEART;
RX
    MEDLINE=97354301; PubMed=9210595;
RA
    Sumathy K., Desai K.V., Kondaiah P.;
    "Isolation of transforming growth factor-beta2 cDNA from a fish,
RT
RT
    Cyprinus carpio by RT-PCR.";
RL
    Gene 191:103-107(1997).
CC
    -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
        DEPENDENT T-CELL GROWTH.
CC
CC
    -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
    -! - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
    EMBL; U66874; AAB62983.1; -.
DR
    HSSP; P08112; 2TGI.
    InterPro; IPR001839; TGFb.
DR
    InterPro; IPR001111; TGFb N.
DR
    InterPro; IPR003911; TGF TGFb.
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    Pfam; PF00688; TGFb_propeptide; 1.
DR
    PRINTS; PR01423; TGFBETA.
DR
    ProDom; PD000357; TGFb; 1.
DR
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    Growth factor; Mitogen; Glycoprotein.
KW
FT
    NON TER
                1
                       1
    PROPEP
                      257
FT
                <1
                      361
                               TRANSFORMING GROWTH FACTOR BETA 2.
FT
    CHAIN
               258
               264
                      273
                               BY SIMILARITY.
FT
    DISULFID
FT
    DISULFID
               272
                      335
                               BY SIMILARITY.
                               INTERCHAIN (BY SIMILARITY).
FT
    DISULFID
               334
                      334
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
               30
                      30
                      98
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
                98
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FΤ
    CARBOHYD
              199
                      199
FT
    NON TER
               361
                     361
    SEQUENCE 361 AA; 41931 MW; 94D930FA970A3FD3 CRC64;
SO
                        31.7%; Score 678.5; DB 13; Length 361;
 Query Match
 Best Local Similarity 40.8%; Pred. No. 1e-51;
 Matches 155; Conservative 55; Mismatches 115; Indels
                                                           55; Gaps
                                                                      14:
          52 QILSKLRLASPPSQGDVPPGP--LPEAVLALYNSTRDRVAGESVEPEPEPE-----ADYY 104
Qу
             Db
           1 QILCKLKLSCPP---EIYPEPEEVSRDIIAIYNSTRDLLQEKANERAATCERQRTGEEYY 57
         105 AKEVTRVLM---VESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL- 160
Qу
             58 AKEVHKIDMQPFYPAENVIPTKHY-NPYFRRLRFDVSSMEKNASN---LVKAELRIFRLQ 113
Db
         161 --KLKV-EQHVELYQ-----KYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRRE 212
QУ
               114 NPKARVSEQRIELYQILGHKDLTSPTQRYIDSKVVRTRTEGEWLSFDVTEAVSEWLLHRD 173
Db
         213 AIEGFRLSAHSSS-----DSKDNTLHVEINGFNSG--RRGDLATI----HGMNR 255
OУ
```

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: |
                                           1 :
         174 RNNGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDDSFVHGGDLKMFKKRRHSGQS 233
Db
        256 PFLLLMATPLERAOHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVROLYIDF 315
Qу
            Db
         234 PHLLLMLLPSYRLESQHKS-HRO------KRALDAAFCFRNVQDNCCLRSLYIDF 281
         316 RKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALE 375
Qу
            Db
         282 KKDLGWKWIHEPKGYNANFCAGACPYLWSADTQHSNILGLYNTINPEASASPCCVSQDLE 341
         376 PLPIVYYVGRKPKVEQLSNM 395
Qу
            [] [:[]:[]:[]:[][]
         342 PLTILYYIGKTPKIEQLSNM 361
Db
RESULT 14
Q95N80
ID
    O95N80
               PRELIMINARY:
                               PRT:
                                     124 AA.
AC
    095N80;
DT
    01-DEC-2001 (TrEMBLrel. 19, Created)
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT
DE
    Transforming growth factor beta 1 (Fragment).
    Canis familiaris (Dog).
OS
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC
OX
    NCBI TaxID=9615;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Fonfara S., Groene A., Baumgaertner W.;
RT
    "Sequence of canine transforming growth factor beta 1 mRNA in DH82-
    cells.";
RT
    Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RL
CC
    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
    EMBL; AF349538; AAK54072.1; -.
DR
    InterPro; IPR001839; TGFb.
DR
DR
    Pfam; PF00019; TGF-beta; 1.
DR
    ProDom; PD000357; TGFb; 1.
    SMART; SM00204; TGFB; 1.
DR
    PROSITE; PS00250; TGF BETA 1; 1.
DR
    NON TER
FT
                1
FT
    NON TER
               124
                     124
    SEQUENCE 124 AA; 14329 MW; 21D185218E5556DB CRC64;
SO
 Query Match
                       31.6%; Score 676.5; DB 6; Length 124;
 Best Local Similarity 89.8%; Pred. No. 3.3e-52;
 Matches 123; Conservative 0; Mismatches 1; Indels 13; Gaps
         264 PLERAQHLHSSRHRRALDTNDYKDDDDKALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKW 323
QУ
            1 PLERAQHLHSSRQRR------ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKW 47
Db
Qу
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DT
     01-JUL-1997 (TrEMBLrel. 04, Created)
DT
     01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
     Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
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GN
OS
     Oryctolagus cuniculus (Rabbit).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX
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RN
     [1]
RP
     SEQUENCE FROM N.A.
RA
     Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
RL
     Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN
RP
     SEQUENCE OF 2-99 FROM N.A.
RA
     Inoue K., Kawabe Y., Kodama T.;
RL
     Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC
     -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC
         PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC
         TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC
         THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC
         REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC
         DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC
     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC
     -! - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR
     EMBL; AF000133; AAB53806.1; -.
DR
     EMBL; AB020217; BAA36950.1; -.
     HSSP; P01137; 1KLA.
DR
DR
     InterPro; IPR002400; GF cysknot.
DR
     InterPro; IPR001839; TGFb.
DR
     Pfam; PF00019; TGF-beta; 1.
DR
     PRINTS; PR00438; GFCYSKNOT.
DR
     ProDom; PD000357; TGFb; 1.
DR
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DR
     PROSITE; PS00250; TGF BETA 1; 1.
KW
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FT
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                   1
                          1
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FT
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                   1
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FT
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                         16
                                  BY SIMILARITY.
FT
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FT
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FT
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                         77
FT
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                   2
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                                  LD -> FS (IN REF. 2).
FT
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SO
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		Similarity							
Matches	112	2; Conservat	cive 0;	Mismatc	hes 0;	Indels	0;	Gaps	0;
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Qy	352	VLALYNQHNPGA						103	
				11111111		1111111111			
Db	61	VLALYNQHNPGA	ASAAPCCVPQ	ALEPLPIVY	YVGRKPKVE(QLSNMIVRSCH	KCS I	112	

Search completed: October 28, 2003, 09:12:26

Job time : 33.3099 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27; Search time 5276.94 Seconds

(without alignments)

10489.161 Million cell updates/sec

Title: US-10-017-372E-34

Perfect score: 1353

Sequence: 1 gatctggtaccgagatggcg.....gattaaagcggccgcgact 1353

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb ba:*

2: gb htg:*

3: gb in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*
14: gb_vi:*

15: em ba:*

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16: em_fun:*

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29: em_vi:*
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31: em_htg_inv:*
32: em_htg_other:*
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^{રુ}

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score	Match	Length	DB	ID	Description
	1226 4	01.4	3206		DICTORDIA	M23703 Sus scrofa
1 2	1236.4	91.4 90.5	3206 1326	4 6	PIGTGFB1A AX338213	AX338213 Sequence
3	1224.6 1217	89.9	1750	4	GGTGFB1	X12373 Porcine mRN
				_		Y00111 Porcine mRN
4	1146.8	84.8	1605	4	SSTGFBR	AF461808 Sus scrof
5 6	1125.4	83.2	2221	4 4	AF461808	L34956 Canine tran
	1005.8	74.3	1369		DOGTGFB1A	E00973 cDNA encodi
7	994.8	73.5	2527	6	E00973	A06669 Synthetic m
8	994	73.5	2537	6	A06669	
9	988	73.0	1173	4	OATGFB1	X76916 O.aries mRN
10	987.6	73.0	1780	9	BC000125	BC000125 Homo sapi
11	987.6	73.0	1780	9	BC001180	BC001180 Homo sapi
12	986.2	72.9	1561	9	AGMTGFB	M16658 Simian tran
13	983.4	72.7	1821	6	E03028	E03028 DNA encodin
14	983	72.7	1746	9	BC022242	BC022242 Homo sapi
15	981.8	72.6	1560	6	106216	106216 Sequence 2
16	981	72.5	2745	9	HSTGFB1	X02812 Human mRNA
17	979.8	72.4	1560	6	108268	I08268 Sequence 2
18	962.4	71.1	1569	6	106221	106221 Sequence 3
19	957.4	70.8	1561	6	I08275	I08275 Sequence 3
20	942.8	69.7	1173	9	BT007245	BT007245 Homo sapi
21	942.8	69.7	1173	12	BT007866	BT007866 Synthetic
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28	876	64.7	1641	10	BC013738	BC013738 Mus muscu
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39	558.8	41.3	699	6	I05434	I05434 Sequence 4
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ALIGNMENTS

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                                                                 MAM 31-MAR-1995
LOCUS
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DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.
ACCESSION
            M23703
VERSION
            M23703.1 GI:755044
KEYWORDS
            transforming growth factor-beta-1.
SOURCE
            Sus scrofa (pig)
  ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
               (bases 1 to 3206)
            Kondaiah, P., Van Obberghen-Schilling, E., Ludwig, R.L., Dhar, R.,
  AUTHORS
            Sporn, M.B. and Roberts, A.B.
            cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
  TITLE
            Evidence for alternate splicing and polyadenylation
            J. Biol. Chem. 263 (34), 18313-18317 (1988)
  JOURNAL
            89054010
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            On Apr 1, 1995 this sequence version replaced gi:341017.
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3186. .3191 polyA signal /gene="TGF-beta-1" 3206 polyA_site /gene="TGF-beta-1" 596 t 1041 c 924 g BASE COUNT 645 a ORIGIN Score 1236.4; DB 4; Length 3206; 91.4%; Query Match Pred. No. 1.5e-208; 96.3%; Best Local Similarity 39; Gaps Matches 1292; Conservative 0; Mismatches 11; Indels 1; Qу Db 70 TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129 Qу 961 TAGTGCTGACGCCTGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGG 1020 Dh 130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189 Qу 1021 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 1080 Db 190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249 Qу 1081 TCGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCCGTACTGG 1140 Db 250 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 309 Qу 1141 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 1200 Db 310 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 369 Qу 1201 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 1260 Db 370 AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG 429 Qу Db 1261 AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG 1320 430 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 489 Qу Db 1321 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 1380 490 GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 549 Qу 1381 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 1440 Db 550 GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG 609 Qу 1441 GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG 1500 Db 610 ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC 669 Qу

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Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG 84	9
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RESULT 2 AX338213

1326 bp DNA linear PAT 09-JAN-2002 LOCUS AX338213

DEFINITION Sequence 1 from Patent WO0181404.
ACCESSION AX338213
VERSION AX338213.1 GI:18128750

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 ORGANISM
         Sus scrofa
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REFERENCE
          Strober, W., Nakamura, K., Kitani, A. and Fuss, I.J.
 AUTHORS
 TITLE
          Inducible plasmid vector encoding tgf- g(b) and uses thereof
 JOURNAL
          Patent: WO 0181404-A 1 01-NOV-2001;
          THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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                            0; Mismatches
                                           9; Indels
                                                       41; Gaps
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QУ
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Db
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LOCUS
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DEFINITION Porcine mRNA for transforming growth factor-beta 1.
ACCESSION X12373
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VERSION
          transforming growth factor-beta 1.
KEYWORDS
SOURCE
          Sus scrofa (pig)
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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             (bases 1 to 1750)
REFERENCE
          Jakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
 AUTHORS
 TITLE
          Nucleotide sequence of chicken transforming growth factor-beta 1
          (TGF-beta 1)
 JOURNAL
          Nucleic Acids Res. 16 (17), 8730 (1988)
         88335639
 MEDLINE
          3166520
  PUBMED
REFERENCE
            (bases 1 to 1750)
 AUTHORS
          Jakowlew, S.B.
 TITLE
          Direct Submission
          Submitted (14-JUL-1988) Jakowlew S.B., National Institute of
 JOURNAL
          health, National Cancer Institute, Laboratory of Chemoprevention,
          Building 41, Room B902, Bethesda, Maryland 20892, USA
COMMENT
          The submitters believe that the chicken cDNA library was
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ACCESSION
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VERSION
KEYWORDS
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REFERENCE
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 AUTHORS
          Derynck, R. and Rhee, L.
          Sequence of the porcine transforming growth factor-beta precursor
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          Nucleic Acids Res. 15 (7), 3187 (1987)
 JOURNAL
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DEFINITION Sus scrofa transforming growth factor beta 1 (TGFB1) mRNA, complete
ACCESSION
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VERSION
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REFERENCE
            (bases 1 to 2221)
 AUTHORS
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
 TITLE
          Polymorphism in the porcine transforming growth factor beta 1 gene
 JOURNAL
          Unpublished
            (bases 1 to 2221)
REFERENCE
 AUTHORS
          Wimmers, K., Chomdej, S., Ponsuksili, S. and Schellander, K.
          Direct Submission
 TITLE
 JOURNAL
          Submitted (20-DEC-2001) Institute of Animal Breeding Science,
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REFERENCE AUTHORS	1	ammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. (bases 1 to 1369) anning,A.M., Auchampach,J.A., Drong,R.F. and Slightom,J.L.	

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Cloning of a canine cDNA homologous to human transforming growth
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 JOURNAL
          Unpublished (1994)
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TITLE

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ACCESSION
VERSION
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REFERENCE
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 AUTHORS
          Riku, M.A.D.D. and Debitsudo, B.G.
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          Patent: JP 1986219395-A 1 29-SEP-1986;
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A06669

LOCUS A06669 2537 bp mRNA linear PAT 29-JUL-1993

DEFINITION Synthetic mRNA for preTGF-Betal. ACCESSION A06669

VERSION A06669.1 GI:412940

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ACCESSION
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VERSION
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           Bovidae; Caprinae; Ovis.
REFERENCE
 AUTHORS
           Woodall, C.J., McLaren, L.J. and Watt, N.J.
 TITLE
           Sequence and chromosomal localisation of the gene encoding ovine
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 JOURNAL
           Gene 150 (2), 371-373 (1994)
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REFERENCE
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 AUTHORS
           Woodall, C.
           Direct Submission
 TITLE
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 JOURNAL
           Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
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REFERENCE	1	ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 1780)	
AUTHORS TITLE JOURNAL	Di Su Ge In	rausberg,R. Frect Submission Ubmitted (03-NOV-2000) National Institutes of Health, Mammalia Ene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590	
REMARK		H-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT		ontact: MGC help desk mail: cgapbs-r@mail.nih.gov	

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DNA Sequencing by: Genome Sequence Centre,
          BC Cancer Agency, Vancouver, BC, Canada
           info@bcqsc.bc.ca
          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
          Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
          Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
          Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
          Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
          Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
          Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
          George Yang, Scott Zuyderduyn, Marco Marra.
          Clone distribution: MGC clone distribution information can be found
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Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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BC001180 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	EDN H	Homo sapiens, Similar to transforming growth factor, beta 1, clone MGC:2323 IMAGE:3356605, mRNA, complete cds. BC001180 BC001180.1 GI:12654682 MGC. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: e Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 37097.

Location/Qualifiers
1. .1780

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1. .1780

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VERSION
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REFERENCE
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          Ohashi, H., Ishii, Y., Miyata, Y., Miyazono, K., Miyagawa, K. and
 AUTHORS
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          PRODUCTION OF HUMAN PRO-TGF-BETA1 BY GENETIC RECOMBINATION
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 AUTHORS
          Strausberg, R.
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          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          NIH-MGC Project URL: http://mgc.nci.nih.gov
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          Contact: MGC help desk
COMMENT
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          Web site:
                       http://www-shqc.stanford.edu
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Contact: (Dickson, Mark) mcd@paxil.stanford.edu

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Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.

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7	992.4	73.3	2537	15	AAQ56923	Human pre-TGF-beta
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  42
       591.4
               43.7
                     1352
                           24 ABK90342
                                                        DNA encoding mIFNB
  43
       589.8
              43.6
                     1350 24 ABK90343
                                                        DNA encoding huIFN
  44
         538
               39.8 875 23 AAS70979
                                                        DNA encoding novel
  45
       366.4 27.1
                      489 24 ABL99528
                                                        Target canine gene
```

ALIGNMENTS

```
RESULT 1
AAD22696
     AAD22696 standard; cDNA; 1326 BP.
XX
AC
     AAD22696;
XX
DT
     26-FEB-2002 (first entry)
XX
DE
     Porcine transforming growth factor beta 1 (TGF-beta1) cDNA.
XX
KW
     Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW
     IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW
     multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW
     diabetes mellitus; sarcoidosis; psoriasis; dermatological; ss.
XX
OS
     Sus scrofa.
XX
FH
                     Location/Qualifiers
     Key
FT
     CDS
                     16..1188
                     /*tag=a
FT
FT
                     /product= "Porcine TGF-betal mutant protein"
XX
PN
     WO200181404-A2.
XX
PD
     01-NOV-2001.
XX
ΡF
     20-APR-2001; 2001WO-US12980.
XX
PR
     20-APR-2000; 2000US-199014P.
ХX
PA
     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PΙ
     Strober W, Nakamura K, Kitani A, Fuss IJ;
XX
```

```
DR
    WPI; 2002-026155/03.
DR
    P-PSDB; AAE13596.
XX
PT
    Composition for treating autoimmune diseases e.g. inflammatory bowel
PT
    disease in humans, comprises vector containing transforming growth
PT
    factor-beta under the control of inducible promoter
XX
PS
    Claim 1; Fig 1; 78pp; English.
XX
CC
    The invention relates to a composition containing a vector comprising a
CC
    gene encoding a regulatory transcription factor under the control of a
CC
    promoter encoding a transforming growth factor-beta (TGF-beta). The
CC
    vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2
CC
    or TGF-beta3, its variants or homologues, by transfecting a cell which
CC
    is part of a host suspected of having an autoimmune disease, especially
CC
    inflammatory bowel disease (IBD), under conditions such that the
CC
    polypeptide encoded by the nucleic acid sequence in the vector is
CC
    expressed. The vector is delivered using a delivery system. The delivery
CC
    of the vector results in substantial elimination of symptoms of the
CC
    autoimmune disease and increased production of IL-10 by the host. The
    composition is useful for treating various diseases with an autoimmune
CC
CC
    component such as multiple sclerosis, rheumatoid arthritis, systemic
CC
    lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC
    and psoriasis, and also for assaying the expression of a gene in a cell.
CC
    The vector is further useful for screening of the effect of test
CC
    compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC
    The present sequence is a cDNA encoding porcine TGF-betal mutant.
XX
SO
    Sequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other;
 Query Match
                       90.5%; Score 1224.6; DB 24; Length 1326;
 Best Local Similarity
                      96.3%; Pred. No. 3.7e-241;
 Matches 1301; Conservative
                           0; Mismatches
                                          9; Indels
                                                        41; Gaps
                                                                   3;
          1 GATCTGGTACCGAGATGGCGCCTTCGGGGGCTGCGGGCTCTTGCCGCTGCTGCCGCTGC 60
Qу
            2 GATCTGGTACCGAGATGCCGCCTTCGGGGCTGCTGCCGCTGCTGCCGCTGCCGCTGC 61
Db
         61 TGTGGCTGCTGGCGGCCGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCA 120
Qу
            62 TGTGGCTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCA 121
Db
        121 TCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCCATTCGCGGCCAGATTCTGTCCA 180
Qу
            122 TCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCA 181
Db
        181 AGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGCCGGCCCGGCCCGCTGCCTGAGG 240
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            Db
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              Db
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        301 AGCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAA 360
Qу
            Db
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302 AGCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAA 361

Qу	361	GCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCA 420
Db	362	GCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCA 421
Qy	421	ACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGC 480
Db	422	ACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGC 481
Qy	481	GCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCA 540
Db	482	GCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCA 541
Qy	541	ATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGC 600
Db	542	ATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGC 601
Qу	601	TGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGG 660
Db	602	TGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGG 661
Qy	661	GTTTTCGCCTCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAA 720
Db	662	GTTTTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAA 721
Qу	721	TTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGC 780
Db	722	TTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGC 781
Qy	781	CCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGC 840
Db	782	CCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCCAGCACCTGCACAGCTCCCGGC 841
Qy	841	ACCGCCGAGCCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCA 900
Db	842	ACCGCCGAGCCCTGGATACCA 862
Qy	901	ACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG
Db	863	ACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG
Qy	961	GGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCC 1020
Db	923	GGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCC 982
Qy	1021	TGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGT 1080
Db	983	TGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGT 1042
Qy	1081	ACAACCAGCACAACCCGGGCGCGCGCGCGCGCGCGCGCG
Db	1043	ACAACCAGCACAACCCGGGCGCGCGCGCGCGCGCGCGCG
Qу	1141	CACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGA 1200
Db	1103	CACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGA 1162

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QУ
        Db
        1163 TCGTGCGTTCCTGCAAGTGCAGCTGA-GCCCCGCCCGCCCACAGCCCCGCCCACCCGGC 1221
Qу
        1261 AGGCCCGGCCCACCCCGCCCGCCTCACCGGGGCTGTATTTAAGGACATCGTGCCCCAA 1320
            Db
        1222 AGGCCCGGCCCACCCCGCCCGCCTCACCGGGGCTGTATTTAAGGACATCGTGCCCAA 1281
Qу
        1321 GCCCACTTGGGATCGATTAAAGCGGCCGCGA 1351
            Db
        1282 GCCCAC-TGGGATCGATTAAAGGTGGAGAGA 1311
RESULT 2
ABQ76674
ID
    ABQ76674 standard; DNA; 2527 BP.
XX
AC
    ABQ76674;
XX
DT
    26-MAR-2003 (first entry)
XX
    Androgen receptor signalling pathway-associated DNA E00973.
DE
XX
KW
    Androgen receptor; transactivation; modulator; Smad3; Smad4; Akt; TGF-B;
KW
    signal transduction pathway; transforming growth factor-B; phosphatase;
    tensin; cytostatic; antiproliferative; cellular proliferation; cancer;
KW
KW
    E00973; ds.
XX
OS
    Synthetic.
XX
PN
    WO200282081-A2.
XX
PD
    17-OCT-2002.
XX
    05-APR-2002; 2002WO-US11086.
PF
XX
PR
    06-APR-2001; 2001US-282266P.
    13-MAR-2002; 2002US-365060P.
PR
XX
    (UYRP ) UNIV ROCHESTER.
PΑ
XX
PΙ
    Chang C;
XX
DR
    WPI; 2003-046871/04.
XX
PT
    Modulating androgen receptor activity, by administering a compound that
PT
    modulates receptor activity, inhibits receptor-signal transduction
PT
    pathway/receptor-coactivator interaction or changes amount or receptor
PT
XX
    Disclosure; Page 225-226; 302pp; English.
PS
XX
CC
    This invention describes a novel method for modulating androgen receptor
    activity or androgen receptor-mediated transactivation activity in a
CC
CC
    cell. The method involves administering a compound which causes
CC
    modulation of the androgen receptors activity and the inhibition of
CC
    interaction between the receptor and a protein involved in a signal
```

CC transduction pathway. The compound also inhibits the interaction between CC the androgen receptor and a protein selected from Smad3, Smad4, Akt, transforming growth factor (TGF)-B and phosphatase and tensin homologues CC CCdeleted on chromosome 10 (PTEN) or their fragments. The compounds of the CC invention have cytostatic and antiproliferative activity. The obtained composition is useful for treating any disease, where uncontrolled CC CC proliferation or cellular proliferation occurs such as cancer, e.g. CC prostate cancer. This sequence represents the androgen receptor CC transactivation signalling pathway modulator E00973 described in CC the method of the invention. XX Sequence 2527 BP; 472 A; 888 C; 735 G; 432 T; 0 other; SO 73.5%; Score 994.8; DB 25; Length 2527; Ouery Match Best Local Similarity 85.9%; Pred. No. 4e-194; Matches 1144; Conservative 0; Mismatches 147; Indels 2: Qу Db 70 TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129 Qу 897 TGGTGCTGACGCCTGGCCCGCCGGCCGGGGACTATCCACCTGCAAGACTATCGACATGG 956 Db 130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189 Qу 957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016 Db 190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249 Qу 1017 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG 1076 Db 250 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 309 Qу 1077 CCCTCTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGCCGGAGCCCGAGC 1136 Db Qу 310 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 369 1137 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG 1196 Db Qу 370 AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG 429

Qу 490 GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 549 Db 1317 GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT 1376

430 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 489

1257 AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA 1316

Db

Qу

Db

Db

Qу 550 GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG 609 1377 GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG 1436

Qy	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	669
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1496
Qy	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1557	TCACTACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1616
Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy		CCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCT	
Db	1676		1697
Qy	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1698	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	1757
Qу	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1758	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT	1817
Qy	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
Db	1818	GCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGC	1877
Qу	1090	ACAACCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1149
Db	1878	ATAACCCGGGCGCCTCGGCGCGCGCGCTGCCCCA	1937
Qy	1150	TCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT	1209
Db	1938	TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGGAGCTGTCCAACATGATCGTGCGCT	1997
Qy	1210	CCTGCAAGTGCAGCTGAGGCCCCGCCCCACAGCCCCGCCACCCGGCAGGCCCGGC	1269
Db	1998	CCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCGCCCGCCC	2055
Qy	1270	CCCACCCCGCCCGCCTCACCGGGGCTGTATTTAAGGACATCGTGCCCCAAGCCCACTTG	1329
Db	2056	GCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCCCAAGCCCACCTG	2115
Qy	1330	GGATCGATTAAA 1341	
Db	2116	GGGCCCCATTAA 2127	

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AC
    AAN60972:
XX
DT
    31-OCT-2002
                (updated)
DT
    28-OCT-1991 (first entry)
XX
DE
    Sequence encoding preTGF-beta.
XX
KW
    Transforming growth factor beta; cancer; wound healing.
XX
OS
    Unidentified.
XX
FΗ
    Kev
                  Location/Qualifiers
FΤ
    misc structure 37..113
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FT
    CDS
                  842..2014
FT
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FT
    mat peptide
                  1676..2011
FT
                  /*taq=c
XX
PN
    EP200341-A.
XX
    10-DEC-1986.
PD
XX
PF
    21-MAR-1986;
                 86EP-0302112.
XX
PR
    22-MAR-1985;
                 85US-0715142.
PR
    13-MAR-1987;
                 87US-0025423.
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynck RMA;
XX
DR
    WPI; 1986-326875/50.
    P-PSDB; AAP61468.
DR
XX
PT
    TGF-beta prodn. from transformed hosts - useful esp. for treating
PT
    wounds (J6 2/9/86).
XX
PS
    Disclosure; Fig 1b; 26pp; English.
XX
    The gene product is known to stimulate cell proliferation and
CC
CC
    inhibit anchorage-dependent growth of a variety of human cancer cell
    lines, it is esp. useful in treatment of burns and the promotion of
CC
CC
    surface and internal wound healing. TGF-beta may be expressed from a
CC
    transformed CHO cell line.
CC
    (Updated on 31-OCT-2002 to add missing OS field.)
XX
SQ
    Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Query Match
                      73.5%; Score 994; DB 7; Length 2537;
 Best Local Similarity
                      85.7%; Pred. No. 5.8e-194;
 Matches 1148; Conservative
                           0; Mismatches 145; Indels
                                                      47; Gaps
                                                                   2:
Qу
         Db
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Qу	70	TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG	129
Db	897	TGGTGCTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG	956
Qу	130	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC	189
Db	957	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	1016
Qу	190	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	249
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	250	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	309
Db	1077	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC	1136
Qy	310	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC	369
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qу	370	AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG	429
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATAT	1256
Qу	430	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	490	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	1317	GGCTCAAGTTAAAAGTGGAGCACGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qу	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qу	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	669
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1496
Qу	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qу	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1557	TCACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1616
Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
QУ	850	CCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCT	909
Db	1676		1697

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Qу
       970 TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT 1029
          Db
      1758 TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT 1817
Qу
      1030 GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC 1089
          Db
      1818 GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGC 1877
Qу
      1090 ACAACCCGGGCGCGCGCGCGCGCGCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCA 1149
          Db
      1878 ATAACCCGGGCGCCTCGGCGGCGCGCGTGCTGCGTGCCGAGGCGCTGGAGCCGCTGCCCA 1937
Qу
      1150 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT 1209
          Db
      1938 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT 1997
      1210 CCTGCAAGTGCAGCTGAGGCCCCGCCCGCCCACAGCCCCGCCACCCGGCAGGCCCGGC 1269
Qу
           Db
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QУ
          Dh
      2058 CCCGCCCGCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCCCAAG 2117
      1322 CCCACTTGGGATCGATTAAA 1341
Qу
          Dh
      2118 CCCACCTGGGGCCCCATTAA 2137
RESULT 4
AAQ03301
   AAQ03301 standard; DNA; 2537 BP.
XX
AC
   AAQ03301;
XX
DT
   25-MAR-2003
             (updated)
   05-AUG-1990 (first entry)
DT
XX
   cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-
DE
DE
   1).
XX
KW
   Transforming growth factor-beta-1 (TGF-beta-1);
KW
   neoplastic cell line inhibition;
KW
   EGF-potentiated anchorage-independent growth;
XX
OS
   Homo sapiens.
XX
FH
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FT
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   mat peptide
FT
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FT
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FT
    misc feature
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FT
                  /*tag= d
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FT
                  and a downstream TATA-like sequence"
XX
PN
    US4886747-A.
XX
PD
    12-DEC-1989.
XX
PF
    13-MAR-1987;
                87US-0025423.
XX
PR
    13-MAR-1987; 87US-0025423.
XX
PΑ
    (GETH ) GENENTECH INC.
XX
    Derynck RMA, Goeddel DV;
PΙ
XX
DR
    WPI; 1990-051338/07.
    P-PSDB; AAR05258.
DR
XX
    Nucleic acid encoding transforming growth factor-beta -
PТ
РΤ
    cloned into expression vectors for expression in eukaryotic host
PT
    cells for therapeutic use
XX
    Disclosure; Fig 1b; 28pp; English.
PS
XX
CC
    It was obtained by an analysis of several overlapping cDNAs and gene
CC
    fragments, leading to the detn. of a continuous sequence corresp. to the
CC
    TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
    encode biologically active transforming growth factor (TGF-beta),
CC
CC
    operably linked to DNA that encodes a secretory leader (SL). It, or a
CC
    nucleic acid capable of hybridising with it, can also be labelled and
CC
    used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
CC
    proteins.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SO
    Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Query Match
                      73.5%; Score 994; DB 11; Length 2537;
 Best Local Similarity
                      85.7%; Pred. No. 5.8e-194;
 Matches 1148; Conservative 0; Mismatches 145; Indels
                                                      47; Gaps
                                                                  2;
         QУ
                Db
        70 TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129
QУ
            897 TGGTGCTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG 956
Db
Qу
        130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189
            957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016
Db
QУ
        190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249
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Db	1017		1076
Qy	250	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	309
Db	1077		1136
Qy	310	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC	369
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qy	370	AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG	429
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATAT	1256
Qy	430	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	490	GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	1317	GGCTCAAGTTAAAAGTGGAGCACCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qy	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qу	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	669
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1496
Qу	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1497	TTAGCGCCCACTGCTCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1557	TCACTACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1616
Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy		CCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCT	
Db	1676	GCCCTGGACACCAACTATTGCT	1697
Qy	910	TCAGCTCCACGGAGAACACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1698	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	1757
Qу		TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	
Db	1758	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT	1817
QУ	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089

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Qу
       1878 ATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCGCAGGCGCTGGAGCCGCTGCCCA 1937
Db
Qу
       1150 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT 1209
           Db
       1938 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT 1997
       1210 CCTGCAAGTGCAGCTGAGGCCCCGCCCGCCCACAGCCCCGCCACCCGGCAGGCCCGGC 1269
QУ
           Db
      1270 CCCACCCCGCCCGCCT------CACCGGGGCTGTATTTAAGGACATCGTGCCCCAAG 1321
Qу
          Db
       2058 CCCGCCCGCCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCCCAAG 2117
      1322 CCCACTTGGGATCGATTAAA 1341
QУ
           Db
      2118 CCCACCTGGGGCCCCATTAA 2137
RESULT 5
AA002814
ID
   AAQ02814 standard; cDNA; 2537 BP.
XX
AC
   AAQ02814;
XX
              (updated)
ПΤ
   25-MAR-2003
   31-OCT-2002
              (updated)
DT
DT
   31-MAY-1989
              (first entry)
XX
   Sequence of pre-TGF-betal cDNA.
DE
XX
KW
   Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW
   inhibition.
XX
OS
   Homo sapiens.
XX
FΗ
                Location/Qualifiers
   Key
FT
   CDS
                842..2011
FT
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FT
                /label=pre-TGF beta 1
FT
   CDS
                1677..2011
FT
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FT
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FT
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FT
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FT
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1818 GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGC 1877

Db

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XX
PN
    WO8912101-A.
XX
PD
    14-DEC-1989.
XX
PF
    08-JUN-1988;
                88WO-US01945.
XX
PR
    08-JUN-1988;
                88WO-US01945.
XX
PΑ
    (GETH ) GENENTECH INC.
XX
ΡI
    Dernyck RMA, Goeddel DV;
XX
DR
    WPI; 1990-007474/01.
DR
    P-PSDB; AAR04034.
XX
PT
    Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT
    probe, or to produce TGF beta 3, for growth inhibition of certain normal
PΤ
    and neoplastic cells, eq A549.
XX
PS
    Disclosure; Fig. 1b; 61pp; English.
XX
CC
    Sequence encodes the 390 amino acid (AA) precursor transforming growth
CC
    factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of
    the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of
CC
CC
    potential secondary structure. The TATA-like sequence in the 3' untrans-
CC
    lated region of the gene is presumably a polyadenylation signal. Mature
CC
    TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is
CC
    cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic
CC
    acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a
CC
    probe or to produce TGF-beta 3 for inhibition of growth of normal and
CC
    neoplastic cells.
CC
    (Updated on 31-OCT-2002 to add missing OS field.)
CC
    (Updated on 25-MAR-2003 to correct PR field.)
CC
    (Updated on 25-MAR-2003 to correct PI field.)
XX
SO
    Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
 Query Match
                      73.5%; Score 994; DB 11; Length 2537;
 Best Local Similarity
                     85.7%; Pred. No. 5.8e-194;
 Matches 1148; Conservative 0; Mismatches 145; Indels
                                                      47; Gaps
                                                                 2;
Qу
         Db
         70 TAGTGCTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129
Qу
            897 TGGTGCTGACGCCTGGCCCGCCGGCCGGGGACTATCCACCTGCAAGACTATCGACATGG 956
Db
Qу
        130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189
            Db
        957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016
Qу
        190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249
            Db
       1017 TCGCCAGCCCCCGAGCCAGGGGGGGGGGCCGCCCGGCCCGCCCGAGGCCGTGCTCG 1076
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Qу	250	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	309
Db	1077		1136
Qy	310	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC	369
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qу	370	AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG	429
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACACGCATATATAT	1256
Qу	430	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qу	490	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	1317	GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qу	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qу	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	669
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1496
Qу	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1557	TCACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1616
Qу	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qу	850	CCCTGGATACCAACGACTACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCT	909
Db	1676		1697
Qy	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1698	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	1757
Qy	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1758	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT	1817
Qу	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
Db	1818	GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCCAGGCCCTGTACAACCAGC	1877

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Qу
       1090 ACAACCCGGGCGCGTCGGCGCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCA 1149
            Db
       1878 ATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCGCTGCCCA 1937
       1150 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT 1209
Qу
            Db
       1938 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT 1997
       1210 CCTGCAAGTGCAGCTGAGGCCCCGCCCACAGCCCCGCCCACCCGGCAGGCCCGGC 1269
QУ
            Db
       1270 CCCACCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACATCGTGCCCCAAG 1321
Qу
                                2058 CCCGCCCGCCCCCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCCCAAG 2117
Db
       1322 CCCACTTGGGATCGATTAAA 1341
QУ
            Db
       2118 CCCACCTGGGGCCCCATTAA 2137
RESULT 6
AAT15720
ID
    AAT15720 standard; cDNA; 2537 BP.
XX
AC
    AAT15720;
XX
DT
    25-MAR-2003
               (updated)
DT
    24-JUL-1997
               (revised)
    25-JAN-1980
DT
              (first entry)
XX
DE
    Pre-transforming growth factor beta 1 cDNA.
XX
    transforming growth factor beta 1; wound healing;
KW
KW
    recombinant production; ss.
XX
OS
    Homo sapiens.
XX
FH
    Key
                 Location/Qualifiers
FT
    5'UTR
                 1..841
FT
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FT
    misc feature
                 37..113
FT
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FT
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FT
                        similar to structural organisation of c-myc RNA,
FT
                        could play role in mRNA stability or in
FT
                        regulation of transcription"
FT
    CDS
                 842..2014
FT
                 /*tag= c
                 /product= pre-TGF_beta_1
FT
FT
    mat peptide
                 1676..2011
FT
                 /*tag= d
FT
                 /product= mature TGF beta 1
FT
    repeat region
                 2015..2100
FT
                 /*tag= e
FT
                 /note= "GC-rich region; possibly responsible for the
FT
                        fact 3'UTR of mRNA could not be cloned as cDNA;
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FT
                          may be important for transcription efficiency"
FT
                  2019..2023
    repeat unit
FT
                   /*tag= f
FT
    TATA signal
                  2094..2100
FT
                   /*tag= g
FT
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FT
                          functions a promoter"
FT
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                  2514..2520
FΤ
                   /*tag= h
FT
                   2529..2536
    misc signal
FT
                   /*taq=i
FT
                   /note= "consensus sequence immediately precedes
FT
                          polyA-tail (Benoist et al)"
XX
PN
    US5482851-A.
XX
PD
    09-JAN-1996.
XX
    05-NOV-1993; 93US-0147364.
PF
XX
PR
                87US-0025423.
    13-MAR-1987;
                85US-0715142.
PR
    22-MAR-1985;
                89US-0389929.
PR
    04-AUG-1989;
PR
    04-MAR-1992;
                92US-0845893.
PR
    05-NOV-1993;
                93US-0147364.
XX
PΑ
    (GETH ) GENENTECH INC.
XX
ΡI
    Derynck RMA, Goeddel DV;
XX
DR
    WPI; 1996-076891/08.
    P-PSDB; AAR90827.
DR
XX
PT
    New recombinant human transforming growth factor-beta prods. - produced
PT
    using Chinese hamster ovary cells, for use in diagnostic applications
PΤ
    or in therapy
XX
PS
    Example 3; Fig 1; 26pp; English.
XX
CC
    The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
CC
    The nucleotide sequence was obtd. by an analysis of several overlapping
CC
    cDNAs and gene fragments. The DNA is useful for the recombinant
    production of TGF beta 1, which can be used in, e.g. wound healing.
CC
CC
    (Revised entry submitted to correct sequence analysis breakdown.)
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
    Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
SO
 Query Match
                       73.5%; Score 994; DB 17; Length 2537;
 Best Local Similarity
                       85.7%; Pred. No. 5.8e-194;
 Matches 1148; Conservative
                            0; Mismatches 145; Indels
                                                         47; Gaps
                                                                     2;
Qу
         Db
QУ
         70 TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129
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Db	897		956
Qy	130	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC	189
Db	957		1016
Qy	190	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	249
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	250	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	309
Db	1077	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC	1136
Qy	310	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC	369
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qу	370	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	429
Db	1197	AAATCTATGACAAGTTCAAGCAGGAGTACACACAGCATATATAT	1256
Qy	430	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	490	GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	1317	GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qy	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qу	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCC	669
Db	1437	ATGTCACCGGAGTTGTGCGCCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1496
Qу		TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qу		TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	
Db		TCACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	
Qy		TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	
Db		TTCTCATGGCCACCCGGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	
Qy 		CCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCT	
Db	1676	occionaled Military	
Qу	910	TCAGCTCCACGGAGAACACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969

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Qу
        970 TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT 1029
           1758 TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT 1817
Db
Qу
       1030 GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC 1089
           1818 GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGC 1877
Db
       1090 ACAACCCGGGCGCGTCGCGCGCGCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCA 1149
Qу
           Db
       1878 ATAACCCGGGCGCCTCGGCGCGCGCGTGCTGCGTGCCGAGGCGCTGGAGCCGCTGCCA 1937
       1150 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT 1209
Qу
           Db
       1938 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT 1997
       1210 CCTGCAAGTGCAGCTGAGGCCCCGCCCGCCCACAGCCCCGCCACCCGGCAGGCCCGGC 1269
Qу
           Db
       1270 CCCACCCCGCCCGCCT------CACCGGGGCTGTATTTAAGGACATCGTGCCCCAAG 1321
Qу
           111 1111 111 11
                                 Db
       2058 CCCGCCCCGCCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCCCAAG 2117
       1322 CCCACTTGGGATCGATTAAA 1341
Qу
           2118 CCCACCTGGGGCCCCATTAA 2137
Dh
RESULT 7
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ΙD
XX
AC
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XX
DT
   25-MAR-2003
              (updated)
DT
   09-JUL-1994
              (first entry)
XX
DE
   Human pre-TGF-beta-1.
XX
KW
   TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW
   transforming growth factor beta-3; recombinant; wound healing;
KW
   vulnerary; ss.
XX
os
   Homo sapiens.
XX
FH
   Key
                Location/Qualifiers
FT
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FT
                /*tag= a
FT
                /note= "possible hairpin loop region"
FT
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                842..2014
FT
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FT
                1676..2011
   mat peptide
FT
                /*tag= c
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                2515..2521
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1698 TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC 1757

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PD
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    04-MAR-1992;
                92US-0845893.
XX
PR
    22-MAR-1985;
                85US-0715142.
PR
    13-MAR-1987;
                87US-0025423.
PR
    04-AUG-1989;
                89US-0389929.
PR
    04-MAR-1992:
                92US-0845893.
XX
PA
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynk RMA, Goeddel DV;
XX
DR
    WPI; 1994-056343/07.
    P-PSDB: AAR46227.
DR
XX
PT
    Nucleic acid sequences encoding transforming growth factor-beta -
PT
    diagnostic probes, and for use in therapeutics
XX
PS
    Disclosure; Fig 1b; 25pp; English.
XX
    cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC
CC
    pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC
    corresponding amino acid sequences were determined (AAR46227-29,
CC
    respectively). A genomic fragment corresponding to a human TGF-
CC
    beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC
    determined (AAR46230). The sequences have been used in the
CC
    construction of vectors for the expression of recombinant TGF-
CC
    beta.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ
    Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
                     73.3%; Score 992.4; DB 15; Length 2537;
 Query Match
 Best Local Similarity
                     85.6%;
                            Pred. No. 1.2e-193;
 Matches 1147; Conservative
                           0; Mismatches 146; Indels
                                                     47; Gaps
                                                               2;
Qу
         Db
        70 TAGTGCTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129
Qу
           Db
        897 TGGTGCTGACGCCTGGCCCGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGG 956
        130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189
Qу
           Db
        957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016
        190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249
Qу
           1017 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG 1076
Db
```

Qу	250	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGGAAAGTGTCGAACCGGAGCCCGAGC	309
Db	1077		1136
Qy	310	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC	369
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qy	370	AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG	429
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACACACATCATATATGTTCTTCAACACATCAG	1256
Qy	430	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	490	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	1317	GGCTCAAGTTAAAAGTGGAGCACCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qу	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qу	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCC	669
Db	1437	ATGTCACCGGAGTTGTGCGCCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1496
Qy	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1616
Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy		CCCTGGATACCAACGACTACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCT	
Db	1676		1697
Qy	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1698	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	1757
Qy	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1758	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT	1817
Qy	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
Db	1818	GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCCAGGTCCTGGCCCTGTACAACCAGC	1877
Qy	1090	ACAACCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1149

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Db
       1150 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT 1209
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           Db
       1938 TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT 1997
QУ
       1210 CCTGCAAGTGCAGCTGAGGCCCCGCCCGCCCACAGCCCGGCCACCCGGCAGGCCCGGC 1269
           Db
       1270 CCCACCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACATCGTGCCCCAAG 1321
Qу
           Db
       2058 CCCGCCCGCCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCCCAAG 2117
Qу
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XX
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XX
DТ
    25-MAR-2003 (updated)
DT
    21-DEC-1998 (first entry)
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    Human pre-transforming growth factor-beta 1 cDNA.
DE
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KW
    Transforming growth factor-beta 1; TGF-beta 1; human; ss.
XX
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    30-MAY-1995;
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XX
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    13-MAR-1987;
               87US-0025423.
PR
    22-MAR-1985;
               85US-0715142.
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PR
    04-AUG-1989;
                89US-0389929.
PR
    04-MAR-1992;
               92US-0845893.
PR
    05-NOV-1993;
                93US-0147364.
PR
    30-MAY-1995:
                95US-0454468.
XX
PΑ
    (GETH ) GENENTECH INC.
XX
PΙ
    Derynck RMA, Goeddel DV:
XX
DR
    WPI; 1998-494840/42.
DR
    P-PSDB; AAW78785.
XX
PT
    DNA encoding transforming growth factor-beta precursor sequence -
PT
    useful for analysis to perform manipulations to increase yield of
PT
    recombinant production of the protein
XX
PS
    Example 3; Fig 1B 1-3; 26pp; English.
XX
CC
    This nucleotide sequence codes for the human transforming growth
CC
    factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC
    composite of overlapping cDNA clones isolated from different cDNA
CC
    libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC
    TGF-beta exon (see AAV52936) restriction fragments as probes.
    The 3' region of the sequence was determined using cloned genomic
CC
    DNA. The invention relates to the recombinant production of
CC
CC
    TGF-beta. Biologically active TGF-beta is defined as being capable
CC
    of inducing EGF-potentiated anchorage independent growth of target
CC
    cell lines and/or growth inhibition of neoplastic cell lines.
CC
    Nucleic acids encoding TGF-beta have been isolated and cloned into
CC
    vectors which are replicated in bacteria and expressed in
CC
    eukaryotic cells. TGF-beta recovered from transformed cells is
CC
    used in known therapeutic applications. TGF-beta nucleic acids are
CC
    also useful in diagnosis and identification of TGF-beta clones.
CC
    (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ
    Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;
 Query Match
                     73.1%; Score 989.2; DB 19; Length 2537;
 Best Local Similarity
                     85.4%; Pred. No. 5.6e-193;
 Matches 1145; Conservative
                         0; Mismatches 148; Indels
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                                                                2;
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           Db
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Qу
           957 AGCAGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016
Db
Qу
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Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qу	370	AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG	429
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Qу	430	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qу	490	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	1317	GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qу	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qу	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCC	669
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGAGAAATTGAGGGCTTTCGCC	1496
Qу	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qу	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1557	TCACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1616
Qу	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qу	850	CCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCT	
Db	1676		1697
Qy	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1698	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	1757
Qy	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1758	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT	1817
Qy	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
Db	1818	GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCCAGGCCCTGTACAACCAGC	1877
Qу	1090	ACAACCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1149

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Db
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          Db
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Qу
       1210 CCTGCAAGTGCAGCTGAGGCCCCGCCCGCCCACAGCCCGGCCAGCCCGGCAGGCCCGGC 1269
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Оv
          Db
       2058 CCCGCCCCGCCCCCGCTGCCTTGCCCATGGGGGGCTGTATTTAAGGACACCGTGCCCCAAG 2117
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       1322 CCCACTTGGGATCGATTAAA 1341
          2118 CCCACCTGGGGCCCCATTAA 2137
Dh
RESULT 9
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   AAQ03268;
XX
   25-MAR-2003 (updated)
DT
DT
   12-AUG-1990 (first entry)
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XX
KW
   Transforming growth factor-beta; psoriasis; TGF-beta; ss.
XX
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XX
PΑ
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XX
PΙ
   Twardzik DR, Purchio AF, Ranchalis JE, Stevens V:
XX
DR
   WPI; 1990-038499/06.
   P-PSDB; AAR03743.
DR
XX
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```
Inhibition of proliferation of epidermal cells -
PT
   used to treat psoriasis by contacting cells with compositions
PT
   containing transforming growth factor-beta.
XX
PS
   Disclosure; fig 1; 20pp; English.
XX
CC
   TGF-beta may be used in the treatment of hyperplasia
CC
   associated with acanthosis-categorised skin diseases, and
CC
   in alleviating psoriatic symptoms associated with cytokine-
CC
   induced phenomena. See also AAQ03269 and AAR03750.
CC
   (Updated on 25-MAR-2003 to correct PA field.)
XX
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   Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
                  72.9%; Score 986.2; DB 11; Length 1561;
 Query Match
 Best Local Similarity 85.8%; Pred. No. 2.1e-192;
 Matches 1150; Conservative
                       0; Mismatches 143; Indels
                                             48; Gaps
                                                       3;
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Qу
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          Db
       377 AGCTGGTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 436
       190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249
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PΤ

Qy	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCC	669
Db	857	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCC	916
Qу	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	917	TTAGCGCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGT	976
Qу	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	977	TCACTACCGGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGC	1036
Qy	790	TCCTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
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Qy	850	CCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCT	909
Db	1096	GCCCTGGACACCAACTACTGCT	1117
Qy	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1118		1177
Qy	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1178	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCT	1237
Qy	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
Db	1238		1297
Qy	1090	ACAACCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1149
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Qy	1150	TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT	1209
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Qy	1210	CCTGCAAGTGCAGCTGAGGCCCGCCCCGCCCACAGCCCCGCCACCCGGCAGGCCCGGC	1269
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Db	1478	CCCACCCCACCCCGCTGTCTTGCCCTTGGGGGCTGTATTTAAGGACACCCGTGCCCCAA	1537
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     AAI58342;
XX
DT
     22-OCT-2001 (first entry)
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     Human polynucleotide SEQ ID NO 545.
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     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW
     peripheral nervous system; neuropathy; central nervous system; CNS;
KW
     Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW
     amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW
     chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW
     leukaemia; ss.
XX
OS
     Homo sapiens.
XX
PN
     WO200153312-A1.
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PD
     26-JUL-2001.
XX
PF
     26-DEC-2000; 2000WO-US34263.
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PR
     21-JAN-2000; 2000US-0488725.
PR
     25-APR-2000; 2000US-0552317.
     09-JUL-2000; 2000US-0598042.
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PR
     19-JUL-2000; 2000US-0620312.
     03-AUG-2000; 2000US-0653450.
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     14-SEP-2000; 2000US-0662191.
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     19-OCT-2000; 2000US-0693036.
PR
     29-NOV-2000; 2000US-0727344.
XX
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     (HYSE-) HYSEQ INC.
XX
ΡI
     Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
     Wang J, Wang Z, Wehrman T, Xu C, Xue AJ,
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                                                  Yang Y, Zhang J;
PΙ
     Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR
    WPI; 2001-442253/47.
     P-PSDB; AAM39186.
DR
XX
PT
    Novel nucleic acids and polypeptides, useful for treating disorders
PT
     such as central nervous system injuries -
XX
PS
     Claim 1; SEQ ID NO 545; 10078pp; English.
XX
CC
     The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC
     the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC
     immunosuppressant and cytostatic activity. The polynucleotides are useful
CC
     in gene therapy. A composition containing a polypeptide or polynucleotide
CC
     of the invention may be used to treat diseases of the peripheral nervous
CC
     system, such as peripheral nervous injuries, peripheral neuropathy and
CC
     localised neuropathies and central nervous system diseases, such as
CC
    Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
    lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC
CC
    utilisation of the activities such as: Immune system suppression,
CC
    Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC
    and thrombolytic activity, cancer diagnosis and therapy, drug screening,
```

```
CC
   C.N.S disorders.
CC
   Note: The sequence data for this patent did not form part of the printed
CC
   specification.
XX
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 Best Local Similarity
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                      Pred. No. 4.9e-192;
 Matches 1149; Conservative
                      0; Mismatches 144;
                                    Indels
                                          48; Gaps
                                                   3;
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QУ
```

assays for receptor activity, arthritis and inflammation, leukaemias and

CC

```
Db
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Db
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          1698 TCAGCTCCACGGAGAGAACTGCTGCGTGCGCAGCTGTACATTGACTTCCGCAAGGACC 1757
Db
       970 TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT 1029
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XX
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XX
DT
   25-MAR-2003 (updated)
DT
   16-APR-1992 (first entry)
XX
DE
   Sequence encoding simian transforming growth factor (TGF) beta-1.
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XX
KW
    Hypertension therapy; hypotensive agent; blood pressure modulator;
KW
XX
OS
    Monkey.
XX
FH
    Key
                  Location/Qualifiers
FT
    CDS
                  262..282
FT
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    sig peptide
                  283..324
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                   /*tag=b
FT
                  325..1098
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FT
                   /*tag= c
FT
                  1099..1436
    mat peptide
FT
                   /*tag= d
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    W09119513-A.
PN
XX
PD
    26-DEC-1991.
XX
PF
    20-JUN-1991;
                91WO-US04449.
XX
PR
    20-JUN-1990; 90US-0541221.
XX
PΑ
    (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PΙ
    Oleson FB, Comereski CR;
XX
    WPI; 1992-024199/03.
DR
DR
    P-PSDB; AAR20124.
XX
PT
    Use of transforming growth factor (TGF)-beta and their
    antagonists - for modulating blood pressure, for treating
PT
PT
    hypertension and hypotension
XX
PS
    Disclosure; Fig 1; 42pp; English.
XX
CC
    A new method for treating hypertension comprises administering a
CC
    transforming growth factor (TGF)-beta to an individual at a dose
CC
    effective for lowering blood pressure; the TGF-beta may be e.g.
CÇ
    mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC
    betal precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC
    beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC
    complex.
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
    Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;
SO
                       72.7%; Score 983.8; DB 13; Length 1559;
 Query Match
 Best Local Similarity
                       85.8%; Pred. No. 6.6e-192;
 Matches 1146; Conservative
                             0; Mismatches 142; Indels
                                                         47; Gaps
                                                                    3;
          Qу
            Db
         75 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 134
Оv
```

Db	321	CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATGGAGCTG	380
Qу	135	GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	194
Db	381	GTGAAGCGGAAGCGATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	440
Qу	195	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	254
Db	441	AGCCCCCGAGCCAGGGGGAGGTGCCGCCGGCCCGGCCCG	500
Qy	255	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG	314
Db	501	TACAACAGCACCCGCGACCGGGTGGCCGGGGGAGAGTGCGGAGCCCGAACCGGAG	560
Qy	315	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	374
Db	561	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	620
Qу	375	TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	434
Db	621	TATGACAAGTTCAAGCAGAGCACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	680
Qу	435	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	494
Db		CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	
Qy	495	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	554
Db		AAGTTAAAAGTCGAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	
Qу		TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	
Db		TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC	
Qу		ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAGT	
Db		ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	
Qу		GCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	
Db		GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	
Qу		TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	-
Db		ACCGGCCGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	
Qу		ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG	
Db		ATGGCCACCCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA	
Qy Db		GATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGC	
		TCCACGGAGAAGAACTGCTGCGTGCGCAGCTCTACATTGACTTCCGGAAGGACCTGGGC	
Qу	313		J 14

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Db
       1122 TCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGC 1181
        975 TGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCC 1034
Qу
           Db
       1182 TGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGGCCCTGTCCC 1241
Qу
       1035 TACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAAC 1094
           1242 TACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAAC 1301
Db
Qу
       1095 CCGGGCGCGTCGGCGCGCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTG 1154
           1302 CCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTG 1361
Db
       1155 TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGC 1214
Qу
           Db
       1362 TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGC 1421
       1215 AAGTGCAGCTGAGGCCCCGCCCCACAGCCCCGCCCACCCGGCAGGCCCGGCCCCAC 1274
Qу
           Db
       1275 CCCCGCCCGC-----CTCACCGGGGCTGTATTTAAGGACA-TCGTGCCCCAAGCCCAC 1326
Qу
           1482 CCACCCCGCTGTCTTGCCCTTGGGGGCTGTATTTAAGGACACCCGTGCCCCAAGCCCAC 1541
Db
       1327 TTGGGATCGATTAAA 1341
Qу
           1542 CTGGGGCCCCATTAA 1556
Db
RESULT 12
AAQ13392
   AAQ13392 standard; DNA; 1821 BP.
XX
AC
   AAQ13392;
XX
DT
   20-NOV-1991 (first entry)
XX
DE
   Human pro-TGF-beta 1 gene.
XX
KW
   Osteogenetic; tumoricidal; ss.
XX
OS
   Homo sapiens.
XX
FH
                Location/Qualifiers
   Key
FT
   CDS
                512..1684
FT
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FT
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                512..598
FT
                /*tag= b
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FT
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                /*tag= e
FT
                /note= "TGF-beta 1"
XX
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ΡN
   JP03180192-A.
XX
PD
   06-AUG-1991.
XX
PF
   07-DEC-1989;
             89JP-0318243.
XX
PR
   07-DEC-1989;
             89JP-0318243.
XX
DΔ
   (KIRI ) KIRIN BREWERY KK.
XX
DR
   WPI; 1991-271579/37.
DR
   P-PSDB; AAR13813.
XX
   Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
PT
PT
   preparing DNA chain contg. base sequence coding for human
PT
   pre:pro-TGF-beta 1, forming expression vector etc.
XX
PS
   Claim 1; Fig 1; 16pp; Japanese.
XX
CC
   The DNA sequence encodes human prepro-TGF-beta 1 which can be
   produced by recombinant methods, it has osteogenetic and
CC
CC
   tumoricidal activity.
XX
SO
   Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;
 Query Match
                  72.7%; Score 983.4; DB 12; Length 1821;
 Best Local Similarity 85.8%; Pred. No. 8.2e-192;
 Matches 1135; Conservative 0; Mismatches 141; Indels
                                              47; Gaps
                                                       2;
        Qу
             Db
       70 TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129
QУ
          567 TGGTGCTGACGCCTGGCCGGCCGGCGGGACTATCCACCTGCAAGACTATCGACATGG 626
Db
Qу
       130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189
          Db
       627 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 686
       190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249
Qу
          Dh
       687 TGGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG 746
       250 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 309
Qу
          Db
       747 CCCTGTACAACAGCACCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 806
Qу
       310 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 369
          807 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG 866
Db
       370 AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG 429
Qу
          Db
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Qу	430	AGCTCCGGGAACCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
Db	927	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	986
Qy	490	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	987	GGCTCAAGTTAAAAGTGGAGCACCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1046
Qу	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
Db	1047	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1106
Qy	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	669
Db	1107	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1166
Qy	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1167	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1226
Qy	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1227	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1286
Qу	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db	1287	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1345
Qу	850	CCCTGGATACCAACGACTACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCT	909
Db	1346		1367
Qу	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1368	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	1427
Qy	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1428	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT	1487
Qy	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
Db	1488	GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCCAGCC	1547
Qy	1090	ACAACCCGGGCGCGTCGGCGCGCGCGCGCGCGCGCGCGCG	1149
Db	1548	ATAACCCGGGCGCCTCGGCGCGCGCGCGCGCGCGCGCGCG	1607
Qу	1150	TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT	1209
Db	1608	TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT	1667
Qу	1210	CCTGCAAGTGCAGCTGAGGCCCCGCCCCACAGCCCCGCCCACCCGGCAGGCCCGGC	1269
Db	1668	CCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCCGCCCCG	1727
Qу	1270	CCCACCCCGCCGCTCACCGGGGCTGTATTTAAGGACATCGTGCCCCAAG	1321

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1728 CCCGCCCGCCCCCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCCCAA 1787
Db
        1322 CCC 1324
Qу
        1788 GCC 1790
Db
RESULT 13
AAN81084
ID
    AAN81084 standard; cDNA; 1560 BP.
XX
AC
    AAN81084;
XX
DT
    25-MAR-2003
                 (updated)
DT
    09-OCT-1990 (first entry)
XX
DE
    Coding sequence of simian transforming growth factor-beta 1.
XX
KW
    Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
    Cercopithecus aethiops.
OS
XX
FH
                    Location/Qualifiers
    Key
                    261..1433
FT
    CDS
                    /*tag=a
FT
FT
    sig peptide
                    282..323
FT
                    /*tag=b
FT
    mat peptide
                    1095..1433
FT
                    /*tag= c
XX
PN
    EP293785-A.
XX
PD
    07-DEC-1988.
XX
PF
    27-MAY-1988; 88EP-0108528.
XX
                 87US-0055662.
PR
    29-MAY-1987;
PR
    25-JAN-1988;
                   88US-0147842.
XX
PA
     (ONCO ) ONCOGEN.
     (BRIM ) BRISTOL-MYERS CO.
PA
XX
    Purchio AG, Gentry L, Twardzik D;
PΙ
XX
DR
    WPI; 1988-347488/49.
    P-PSDB; AAP80647.
DR
XX
PT
     Prodn. of simian transforming growth factor beta-1 - by culturing
PΤ
     transfected eucaryotic cells, and new precursor proteins, useful for
PT
    treating tumours.
XX
PS
    Disclosure; Page ?; pp; English.
XX
    The cDNA is prepd. from African green monkey cell line BSC-40 and is
CC
    expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
CC
    between mature simian and human TGF-beta 1. The plasmid also contains
CC
```

```
CC
   the SV40 promoter and a selection marker, esp. DHFR.
CC
   (Updated on 25-MAR-2003 to correct PA field.)
CC
   (Updated on 25-MAR-2003 to correct PI field.)
XX
SO
   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
                 72.6%; Score 982.8; DB 9; Length 1560;
 Query Match
                 85.8%; Pred. No. 1.1e-191;
 Best Local Similarity
 Matches 1146; Conservative
                      0; Mismatches 142; Indels
                                           48; Gaps
                                                    3;
Qу
       Db
      75 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 134
Qу
         321 CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATCGAGCTG 380
Db
      135 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 194
Qу
         381 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 440
Db
      195 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 254
Qу
         441 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 500
Dh
      255 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 314
Qу
         Db
      315 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 374
Qу
         561 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 620
Db
      375 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 434
Qу
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Db
      435 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC 494
Qу
         681 CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC 740
Db
Qу
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         741 AAGTTAAAAGTCGAGCAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA 800
Db
      555 TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC 614
Qу
         801 TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC 860
Db
      615 ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGGTTTTCGCCTCAGT 674
Qу
         861 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC 920
Db
      675 GCCCACTGTTCCTGTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT 734
Qу
         921 GCCCACTGCTCCTGTGACAGCAAAGATAACACTGCAAGTGGACATCAACGGGTTCACT 980
Db
```

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735 TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC 794
Qу
          981 ACCGGCCGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC 1040
Db
      795 ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG 854
Qy
         Db
      1041 ATGGCCACCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA----- 1094
      855 GATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGC 914
Qу
                               Db
                              -GCCCTGGACACCAACTACTGCTTCAGC 1121
      915 TCCACGGAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGC 974
Qу
         Db
      1122 TCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGC 1181
      975 TGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCC 1034
Qу
         1182 TGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCC 1241
Dh
      1035 TACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAAC 1094
Qу
         1242 TACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAAC 1301
Db
      Qу
         1302 CCGGGCGCCTCGGCGGCGCCGTGCTGCCGCAGGCGCTGGAGCCACTGCCCATCGTG 1361
Db
      1155 TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGC 1214
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Db
      Qу
         Db
      1275 CCCCGCCCGCCT------CACCGGGGCTGTATTTAAGGACA-TCGTGCCCCAAGCCCA 1325
Qу
                         1482 CCCACCCCGCTGTCTTGCCCTTGGGGGCTGTATTTAAGGACACCCGTGCCCCAAGCCCA 1541
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Qу
         | ||| | | | |
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Db
RESULT 14
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T D
XX
AC
   AAQ03508;
XX
DT
   25-MAR-2003
            (updated)
   09-JAN-2003
DT
            (updated)
DT
   14-AUG-1990
            (first entry)
XX
DE
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Simian Transforming growth factor - Betal.

```
XX
KW
    HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW
    factors; ds.
XX
OS
    Cebus apella.
XX
FH
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                 Location/Qualifiers
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FT
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                 1103..1437
FT
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XX
PD
    07-MAR-1990.
XX
PF
    25-AUG-1989; 89EP-0115719.
XX
    25-AUG-1988; 88US-0236698.
PR
XX
    (ONCO ) ONCOGEN LP.
PA
XX
PΙ
    Brankovan V, Lioubin M, Purchio A;
XX
DR
    WPI; 1990-068723/10.
    P-PSDB; AAR05663.
DR
XX
PT
    Compsns. contg. transforming growth factor beta -
PT
    used for inhibitions of HIV infection and replication in vivo.
XX
PS
    Disclosure; Fig 1; 20pp; English.
XX
CC
    TGF-beta may be used in vivo to prevent formation of synctia and
CC
    inhibit HIV infection. TGF may also be used with other HIV treatments
    (AZT, soluble CD4 etc.).
CC
CC
    (Updated on 09-JAN-2003 to add missing OS field.)
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SO
    Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
 Query Match
                     72.6%; Score 982.8; DB 11; Length 1560;
 Best Local Similarity 85.8%; Pred. No. 1.1e-191;
 Matches 1146; Conservative 0; Mismatches 142; Indels 48; Gaps
                                                               3;
         Qу
           Db
         75 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 134
Qу
           Db
        321 CTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATCGAGCTG 380
Qу
        135 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 194
           381 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 440
Db
QУ
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Db	501	TACAACAGCACCCGCGACCGGGTGGCCGGGGGGGGGGGG	560
Qу	315	GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	374
Db	561	GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC	620
Qу	375	TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	434
Db	621	TATGACAAGTTCAAGCAGAGCACACACAGCATATATATGTTCTTCAACACATCAGAGCTC	680
Qу	435	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	494
Db	681	CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	740
Qу	495	AAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	554
Db	741	AAGTTAAAAGTCGAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGA	800
Qy	555	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	614
Db	801	TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC	860
Qу	615	ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	674
Db	861	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	920
Qy	675	GCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	734
Db	921	GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	980
QУ	735	TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	794
Db	981	ACCGGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC	1040
Qу	795	ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG	854
Db	1041	ATGCCACCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA	1094
Qу	855	GATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGC	
Db	1095		1121
Qу	915	TCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGC	974
Db	1122	TCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGC	1181
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KW
    interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW
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KW
    treatment; ds.
KW
XX
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PΑ
XX
ΡI
    Lee M, Perrella MA;
XX
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DR
   WPI: 1995-358443/46.
DR
   P-PSDB; AAR83054.
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PT
   Treatment of hypotension, esp. in septic shock - by administering
PT
   transforming growth factor-beta e.g. to inhibit inducible nitric
PT
   oxide synthase gene transcription
XX
PS
   Disclosure; Fig 15; 52pp; English.
XΧ
CC
   The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which
CC
   has been found to inhibit inducible nitric oxide synthase (iNOS) gene
CC
   transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
CC
   smooth muscle cells, and at a dose which does not inhibit constitutive
CC
   NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
CC
   in the treatment of hypotension, such as that associated with severe
CC
   inflammation or septic shock.
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Job time : 416.484 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 18:35:27; Search time 402.152 Seconds

(without alignments)

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Publication No. US20030119010A1
; GENERAL INFORMATION:
  APPLICANT: Jonsonn, Julie Ruth
  APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
  FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
  NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
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  ORGANISM: Human
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  OTHER INFORMATION:
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; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
  APPLICANT: Ren, Feiyan
  APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
  APPLICANT: Xue, Aidong J.
  APPLICANT: Yang, Yonghong
  APPLICANT: Wang, Jian-Rui
  APPLICANT: Zhou, Ping
  APPLICANT: Ma, Yunqing
  APPLICANT: Wang, Dunrui
  APPLICANT: Wang, Zhiwei
  APPLICANT: Tillinghast, John
  APPLICANT: Drmanac, Radoje T.
  TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
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  FILE REFERENCE: 784CIP2B
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  CURRENT FILING DATE: 2002-01-04
  PRIOR APPLICATION NUMBER: 09/552,317
  PRIOR FILING DATE: 2000-04-25
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  PRIOR FILING DATE: 2000-01-21
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US-10-087-268-4
Sequence 4, Application US/10087268
Publication No. US20030119010A1
GENERAL INFORMATION:
 APPLICANT: Jonsonn, Julie Ruth
 APPLICANT: Powell, Elizabeth Ellen
  TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or
condition
  FILE REFERENCE: Fibrosis
  CURRENT APPLICATION NUMBER: US/10/087,268
  CURRENT FILING DATE: 2002-03-01
 NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
  LENGTH: 1821
  TYPE: DNA
  ORGANISM: Human
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FEATURE:

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NAME/KEY: 5'UTR
  LOCATION: (1)..(511)
  OTHER INFORMATION:
  NAME/KEY: CDS
  LOCATION: (512)..(1684)
  OTHER INFORMATION:
  NAME/KEY: sig peptide
  LOCATION: (512)..(598)
  OTHER INFORMATION:
  NAME/KEY: 3'UTR
  LOCATION: (1685)..(1821)
  OTHER INFORMATION:
US-10-087-268-4
 Query Match
                 72.7%; Score 983.4; DB 14; Length 1821;
 Best Local Similarity 85.8%; Pred. No. 1.6e-254;
 Matches 1135; Conservative
                      0; Mismatches 141; Indels
                                           47: Gaps
                                                    2;
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         567 TGGTGCTGACGCCTGGCCCGCCGGCCGGGGACTATCCACCTGCAAGACTATCGACATGG 626
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      130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189
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         627 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 686
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      190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249
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         687 TCGCCAGCCCCCGAGCCAGGGGGGGGGCCCGCCCGGCCCGGCCCGAGGCCGTGCTCG 746
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Qy	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCC	669
Db	1107	ATGTCACCGGAGTTGTGCGCCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC	1166
Qy	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1167	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1226
Qy	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1227	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC	1286
Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
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Qy		CCCTGGATACCAACGACTACAAGGATGACGACAAGGCCCTGGATACCAACTACTGCT	
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Qy	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
Db	1368	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	1427
Qy	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1428	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCT	1487
Qy	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
Db	1488	GCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGC	1547
Qу	1090	ACAACCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	1149
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Qу	1150	TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT	1209
Db	1608	TCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT	1667
Qу	1210	CCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCCACCCGGCAGGCCCGGC	1269
Db	1668	CCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCCGCCCCG	1727
Qу	1270	CCCACCCCGCCCGCCTCACCGGGGCTGTATTTAAGGACATCGTGCCCCAAG	1321
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Db	1788	GCC 1790	

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; Publication No. US20030050265A1
 GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
  APPLICANT: Susan F. Murray
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                          EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
  PRIOR APPLICATION NUMBER: 60/154,546
  PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
 SEQ ID NO 28
  LENGTH: 2745
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (842)...(2017)
US-09-948-002-28
 Query Match
                  72.5%; Score 981; DB 11; Length 2745;
 Best Local Similarity 85.5%; Pred. No. 7.8e-254;
 Matches 1148; Conservative
                       0; Mismatches 145; Indels
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       250 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 309
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Db
       310 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 369
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          1137 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG 1196
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                         Db
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Db	1317	GGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATT	1376
Qy	547	CCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCT	606
Db	1377	CCTGGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTT	1436
Qу	607	TTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTC	666
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Qy	667	GCCTCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACG	726
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Qy	727	GGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCC	786
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Qy	787	TGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCC	846
Db	1617	TGCTTCTCATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCC	1676
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Qy	907	GCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGG	966
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Qy	967	ACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGC	1026
Db		ACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGC	
Qy	1027	CCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCCAAGGTCCTGGCTCTGTACAACC	1086
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Db	1938	CCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGC	1997
Qy	1207	GTTCCTGCAAGTGCAGCTGAGGCCCCGCCCGCCCACCCGGCCAGGCCC	1266
Db	1998	GCTCCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCCGCC	2057
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US-09-948-002-1
; Sequence 1, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
  APPLICANT: Nicholas M. Dean
  APPLICANT: Susan F. Murray
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                              EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
  CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
  PRIOR APPLICATION NUMBER: 60/154,546
  PRIOR FILING DATE: 1999-09-17
  NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 1
   LENGTH: 2094
   TYPE: DNA
   ORGANISM: Mus musculus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (868)...(2040)
US-09-948-002-1
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 Best Local Similarity
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Qy	610	ATGTCACCGGAGTTGTGCGCCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	669
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Qy	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
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Qy	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	789
Db	1583	TCAGCCCCAAACGTCGGGGCGACCTGGGCACCATCCATGACATGAACCGGCCCTTCCTGC	1642
Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
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Qy	850	CCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCT	909
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Qу	910	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	969
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Qy	970	TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1029
Db	1784	TGGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGTCTG	1843
Qy	1030	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	1089
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       1210 CCTGCAAGTGCAGCTGAGGCCCCGCCCGCCCACAGCCCCGCCCACCCGGCAGGCCCGGC 1269
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           2024 CCTGCAAGTGCAGCTGAAGCCCCGCCCCGC-----CCCGCCCCTCCCGGCAGGCCCGGC 2077
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RESULT 6
US-09-948-002-27
; Sequence 27, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
 APPLICANT: Nicholas M. Dean
  APPLICANT: Susan F. Murray
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
  TITLE OF INVENTION: FACTOR BETA
                             EXPRESSION
  FILE REFERENCE: ISPH-0607
  CURRENT APPLICATION NUMBER: US/09/948,002
 CURRENT FILING DATE: 2000-09-05
  PRIOR APPLICATION NUMBER: 09/661,753
  PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/154,546
 PRIOR FILING DATE: 1999-09-17
 NUMBER OF SEQ ID NOS: 71
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   TYPE: DNA
   ORGANISM: Rattus norvegicus
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (413)...(1585)
US-09-948-002-27
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 Best Local Similarity 82.1%; Pred. No. 1.2e-216;
 Matches 999; Conservative 0; Mismatches 179; Indels
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         70 TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 129
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        468 TAGTGCTGACGCCCGGGAGGCCAGCCGCGGGACTCTCCACCTGCAAGACCATCGACATGG 527
Qу
        130 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 189
           528 AGCTGGTGAAACGGAAGCGCATCGAAGCCATCCGTGGCCAGATCCTGTCCAAACTAAGGC 587
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        190 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 249
Qу
           Db
        588 TCGCCAGTCCCCGAGCCAGGGGGGGGGTACCGCCGGGCCCGCTGCCCGAGGCGGTGCTCG 647
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Qy	250	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	309
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Qу	310	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC	369
Db	708	CCGAGGCGGACTACTACGCCAAAGAAGTCACCCGCGTGCTAATGGTGGACCGCAACAACG	767
Qу	370	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	429
Db	768	CAATCTATGACAAAACCAAAGACATCACACACAGTATATATGTTCTTCAATACGTCAG	827
Qy	430	AGCTCCGGGAAGCGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	489
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Qy	490	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	549
Db	888	GATTCAAGTCAACTGTGGAGCAACACGTAGAACTCTACCAGAAATATAGCAACAATTCCT	947
Qy	550	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	609
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Qy	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	669
Db	1008	ACGTCACTGGAGTTGTCCGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGCT	1067
Qy	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	729
Db	1068	TCAGTGCTCACTGCTCTTGTGACAGCAAAGATAATGTACTCCACGTGGAAATCAATGGGA	1127
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Db	1128	TCAGTCCCAAACGTCGAGGTGACCTGGGCACCATCCATGACATGAACCGACCCTTCCTGC	1187
Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	849
Db		TCCTCATGGCCACCCCCTGGAAAGGGCTCAACACCTGCACAGCTCCAGGCACCGGAGA-	
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Db		GCCCTGGATACCAACTACTGCT	
Qу		TCAGCTCCACGGAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	
Db		TCAGCTCCACAGAGAACTGCTGTGTACGGCAGCTGTACATTGACTTTAGGAAGGA	
Qу		TGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	
Db		TGGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGTCTG	
Qy		GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC	
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RESULT 7
US-09-756-283A-19
; Sequence 19, Application US/09756283A
: Patent No. US20020151478A1
: GENERAL INFORMATION:
 APPLICANT: Chernajovsky, Yuti
  APPLICANT: Dreja, Hanna Stina
  APPLICANT: Adams, Gillian
  TITLE OF INVENTION: Latent Fusion Protein
 FILE REFERENCE: 0623.1000000
  CURRENT APPLICATION NUMBER: US/09/756,283A
  CURRENT FILING DATE: 2001-01-09
 NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
; SEO ID NO 19
  LENGTH: 1376
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: LAP-mIFNbeta construct
   NAME/KEY: CDS
   LOCATION: (1)..(1368)
US-09-756-283A-19
                   48.6%; Score 657.2; DB 10; Length 1376;
 Query Match
 Best Local Similarity 88.3%; Pred. No. 8.3e-167;
 Matches 726: Conservative 0: Mismatches
                                    93: Indels
                                                 3: Gaps
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        Qу
          75 CTGACGCCTGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 134
Qу
          61 CTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGGAGCTG 120
Db
QУ
       135 GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 194
          Db
       121 GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC 180
Qу
       195 AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 254
          Db
       181 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 240
Qу
       255 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 314
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241 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGACTGCAGAACCGGAGCCCGAGCCTGAG 300
Db
       315 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 374
Qу
          Db
       301 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATC 360
Qу
       375 TATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 434
          Db
       361 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 420
Qу
       435 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT---GAGG 491
          421 CGAGAAGCGGTACCTGAACCCGTGTTGCTCCCGGGCAGAGCTGCGTCTGCTGAGGAGG 480
Db
       492 CTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG 551
Qу
          Db
       481 CTCAAGTTAAAAGTGGAGCACCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG 540
       552 CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT 611
Qу
          541 CGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGAT 600
Db
Qу
       612 GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGGGGCTATAGAGGGTTTTCGCCTC 671
          601 GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTT 660
Db
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       672 AGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC 731
          Db
       661 AGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC 720
       732 AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC 791
QУ
          721 ACTACCGGCCGCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTT 780
Db
       792 CTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGC 833
Qу
          Db
       781 CTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGC 822
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US-09-756-283A-21
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; Sequence 21, Application US/09756283A
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; TITLE OF INVENTION: Latent Fusion Protein

; FILE REFERENCE: 0623.1000000

; CURRENT APPLICATION NUMBER: US/09/756,283A

CURRENT FILING DATE: 2001-01-09

; NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn version 3.0

SEQ ID NO 21
LENGTH: 1352
TYPE: DNA

[;] Patent No. US20020151478A1

[;] GENERAL INFORMATION:

[;] APPLICANT: Chernajovsky, Yuti ; APPLICANT: Dreja, Hanna Stina ; APPLICANT: Adams, Gillian

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ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: mIFNbeta-LAP construct
   NAME/KEY: CDS
   LOCATION: (1)..(1344)
US-09-756-283A-21
 Query Match
                   43.9%; Score 594.6; DB 10; Length 1352;
 Best Local Similarity 87.3%; Pred. No. 5.7e-150;
 Matches 664; Conservative
                        0; Mismatches
                                     94;
                                        Indels
                                                3; Gaps
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       137 GAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAG 196
          Db
       642 GAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAG 701
       197 CCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTA 256
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       702 CCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTGTA 761
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Qу
          Db
       762 CAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGC 821
       317 GGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTA 376
Qу
           Db
       822 CGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTA 881
       377 TGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCG 436
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          882 TGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTCCG 941
Db
       437 GGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT---GAGGCT 493
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           942 AGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGAGGCT 1001
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       494 CAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCG 553
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          1002 CAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCG 1061
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Qу
       554 CTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGT 613
           1062 ATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGT 1121
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       614 CACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGGCTATAGAGGGTTTTCGCCTCAG 673
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          1122 CACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAG 1181
Db
       674 TGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAA 733
Qу
           1182 CGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCAC 1241
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       734 TTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCT 793
QУ
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Db
       1242 TACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGCTTCT 1301
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        794 CATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCT 834
           Db
       1302 CATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCT 1342
RESULT 9
US-09-911-904-167
; Sequence 167, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
 APPLICANT: Farr, Spencer B.
 APPLICANT: Pickett, Gavin G.
  APPLICANT: Neft, Robin Eileen
  APPLICANT: Dunn, II, Robert Thomas
  TITLE OF INVENTION: CANINE TOXICITY GENES
 FILE REFERENCE: 400742000200
 CURRENT APPLICATION NUMBER: US/09/911,904
  CURRENT FILING DATE: 2002-04-09
 PRIOR APPLICATION NUMBER: US 60/220,057
  PRIOR FILING DATE: 2000-07-21
  NUMBER OF SEO ID NOS: 386
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
  LENGTH: 489
  TYPE: DNA
   ORGANISM: Canis familiaris
   FEATURE:
   NAME/KEY: misc feature
   LOCATION: (1)...(489)
   OTHER INFORMATION: n = A, T, C or G
US-09-911-904-167
 Query Match 27.1%; Score 366.4; DB 11; Length 489; Best Local Similarity 86.1%; Pred. No. 1.1e-88;
 Matches 445; Conservative 0; Mismatches 32; Indels 40; Gaps
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           1 GACCCTTCCTGCTCCTCATGGCCACCCCACTGGAGAGGGCCCAGCACCTGCACAGCTCCC 60
Db
        838 GGCACCGCCGAGCCCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATA 897
Qу
           61 GGCAGCGCCG-------GGCCCTGGACA 81
Db
        Qу
           Db
         82 CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCTCTACATTGACT 141
Qу
        958 TCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1017
           Db
        142 TCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACCACGCTAACTTCT 201
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       1018 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1077
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       1138 AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1197
            Db
        322 AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCGAACA 381
Qу
       1198 TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCG-CCCACAGCCCCGCCCACC 1256
            Db
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Qу
            Db
        442 CGGCAGGNCCGGCCCCGCCCCGCCGCTGCGCCGGG 478
RESULT 10
US-09-813-271B-1
; Sequence 1, Application US/09813271B
; Patent No. US20020115834A1
   GENERAL INFORMATION:
       APPLICANT:
                 (A) Nico Cerletti
       TITLE OF INVENTION: New process for the production of
                        biologically active protein
       NUMBER OF SEQUENCES: 13
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: No. US20020115834Alartis Patent Department
            STREET: 564 Morris Avenue
            CITY: Summit
            STATE: New Jersey
           COUNTRY: USA
            ZIP: 07901
       COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
       CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/813,271B
            FILING DATE: 20-Mar-2001
       PRIOR APPLICATION DATA:
           APPLICATION NUMBER: PCT/EP95/02719
            FILING DATE: 12-Jul-95
           APPLICATION NUMBER: EPO 94810439.3
           FILING DATE: 25-Jul-94
       ATTORNEY/AGENT INFORMATION:
           NAME: Pfeiffer, Hesna J.
            REGISTRATION NUMBER: 22640
           REFERENCE/DOCKET NUMBER: 4~20039C/C1C1/USN
       TELECOMMUNICATION INFORMATION:
           TELEPHONE: (908) 522-6940
           TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 1:
       SEQUENCE CHARACTERISTICS:
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LENGTH: 339 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
      MOLECULE TYPE: cDNA to mRNA
      HYPOTHETICAL: NO
      IMMEDIATE SOURCE:
          CLONE: E. coli LC137/pPLMu.hTGF-betal (DSM 5656)
      FEATURE:
          NAME/KEY: CDS
          LOCATION: 1..336
          OTHER INFORMATION: /product= "human TGF-betal"
      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1
 Query Match
                   22.8%; Score 308.6; DB 10; Length 339;
 Best Local Similarity 94.4%; Pred. No. 3.5e-73;
 Matches 320; Conservative 0; Mismatches 19; Indels
                                                0; Gaps
                                                         0;
       Qу
          Db
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          61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Db
      1008 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1067
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          Db
       121 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180
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          181 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCCTCGCGGCGCCCTGCTGCCG 240
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      1128 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1187
Qу
          241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
Db
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      1188 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1226
          Db
       301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
RESULT 11
US-09-906-158-3
; Sequence 3, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
  APPLICANT: Brett P. Monia
  APPLICANT: Susan M. Freier
  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
 FILE REFERENCE: RTS-0257
  CURRENT APPLICATION NUMBER: US/09/906,158
  CURRENT FILING DATE: 2001-07-14
  NUMBER OF SEQ ID NOS: 168
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; SEQ ID NO 3
   LENGTH: 2574
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   NAME/KEY: CDS
   LOCATION: (254)...(1492)
US-09-906-158-3
 Query Match
                   17.9%; Score 241.6; DB 11; Length 2574;
 Best Local Similarity 53.8%; Pred. No. 5.9e-55;
 Matches 670; Conservative 0; Mismatches 519; Indels 57; Gaps
                                                         6;
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       100 GACTGTCCACCTGCAAGACCATCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCA 159
Qу
            321 CTCTGTCCACTTGCACCACCTTGGACTTCGGCCACATCAAGAAGAAGAGGGGTGGAAGCCA 380
Db
       160 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGC 219
QУ
          381 TTAGGGGACAGATCTTGAGCAAGCTCAGGCTCACCAGCCCCCTGAGCCAACGGTGATGA 440
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       220 CGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG 279
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          441 CCCACG-----TCCCCTATCAGGTCCTGGCCCTTTACAACAGCACCCGGGAGCTGCTGG 494
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       280 CCGGGGAAAGTGTCGAACCGGAGCCCG------AGCCAGAGGCGGACTACT 324
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       325 ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT 384
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          Db
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       385 TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG 444
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               615 CTGTCTGCCCTAAAGGAATTACCTCCAAGGTTTTCCGCTTCAATGTGTCCTCAGTGGAGA 674
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       445 TGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAG 504
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               675 AAAATAGAACCAACCTATTCCGAGCAGAATTCCGGGTCTTGCGGGTGCCCAACCCCAGCT 734
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       505 TGGAGCACCACGTGGAG------
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            Db
       735 CTAAGCGGAATGAGCAGAGGATCGAGCTCTTCCAGATCCTTCGGCCAGATGAGCACATTG 794
       544 ATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGT 603
Qу
               795 CCAAACAGCGCTATATCGGTGGCAAGAATCTGCCCACACGGGGCACTGCCGAGTGGCTGT 854
Db
       604 CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT 663
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                        855 CCTTTGATGTCACTGACACTGTGCGTGAGTGGCTGTTGAGAAGAGAGTCCAACTTAGGTC 914
Db
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       915 TAGAAATCAGCATTCACTGTCCATGTCACACCTTTCAGCCCAATGGAGATATCCTGGAAA 974
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          Db
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       778 GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCC 837
Qу
                                      1035 GTGGAGATCTGGGGCGCCTCAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCCTCA 1094
Db
       838 GG-----CACCGCCGAGCCCTGGATACCAACGACTACAAGGATGACGACGACAA---GG 888
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                        \perp
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      1095 TGATGATTCCCCCACACCGGCTCGACAACCCGGGCCAGGGGGGGTCAGAGGAAGAAGCGGG 1154
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       949 ACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATG 1008
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      1215 ACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTATG 1274
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          Db
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US-10-028-158-20

- ; Sequence 20, Application US/10028158
- ; Publication No. US20020110833A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Caniggia, Isabella
- ; APPLICANT: Post, Martin
- ; APPLICANT: Lye, Stephen
- ; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
- ; TITLE OF INVENTION: TROPHOBLAST
- FILE REFERENCE: 11757.38USWO
- ; CURRENT APPLICATION NUMBER: US/10/028,158
- CURRENT FILING DATE: 2001-12-20
- ; PRIOR APPLICATION NUMBER: US/09/380,662
- ; PRIOR FILING DATE: 1999-12-21
- ; PRIOR APPLICATION NUMBER: PCT/CA98/00180

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PRIOR APPLICATION NUMBER: US 60/039,919
  PRIOR FILING DATE: 1997-03-07
 NUMBER OF SEQ ID NOS: 24
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
  LENGTH: 2574
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
   NAME/KEY: CDS
  LOCATION: (254)..(1492)
US-10-028-158-20
 Query Match
                   17.9%; Score 241.6; DB 13; Length 2574;
 Best Local Similarity 53.8%; Pred. No. 5.9e-55;
 Matches 670; Conservative 0; Mismatches 519; Indels 57; Gaps
                                                          6;
        QУ
                   261 TGCACTTGCAAAGGGCTCTGGTGGTCCTGGCCCTGCTGAACTTTGCCACGGTCAGCCTCT 320
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       220 CGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG 279
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          441 CCCACG-----TCCCCTATCAGGTCCTGGCCCTTTACAACAGCACCCGGGAGCTGCTGG 494
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       280 CCGGGGAAAGTGTCGAACCGGAGCCCG------AGCCAGAGGCGGACTACT 324
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            1 111 111 111
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PRIOR FILING DATE: 1998-03-05

Qу	604	CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT	663
Db	855	CCTTTGATGTCACTGACACTGTGCGTGAGTGGCTGTTGAGAAGAGAGTCCAACTTAGGTC	914
Qy	664	TTCGCCTCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGG	717
Db	915	TAGAAATCAGCATTCACTGTCCATGTCACACCTTTCAGCCCAATGGAGATATCCTGGAAA	974
Qу	718	AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACC	777
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Qу	778	GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCC	837
Db	1035	GTGGAGATCTGGGGCGCCTCAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCCTCA	1094
Qу	838	GGCACCGCCGAGCCCTGGATACCAACGACTACAAGGATGACGACGACAAGG	888
Db	1095	TGATGATTCCCCCACACCGGCTCGACAACCCGGGCCAGGGGGGTCAGAGGAAGAAGCGGG	1154
Qу	889	CCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	948
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Qу	949	ACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATG	1008
Db	1215	ACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTATG	1274
Qy	1009	CCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGG	1068
Db	1275	CCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACACCCACAGCACGG	1334
Qy	1069	TCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGTGCTGCCGC	1128
Db	1335	TGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCC	1394
Qу	1129	AGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGC	1188
Db	1395	AGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAGC	1454
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US-09-957-458B-9

- ; Sequence 9, Application US/09957458B
- ; Publication No. US20030166271A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Chen, Una
- ; TITLE OF INVENTION: Method for growing stem cells
- ; FILE REFERENCE: P66567US0
- ; CURRENT APPLICATION NUMBER: US/09/957,458B
- ; CURRENT FILING DATE: 2001-09-21
- ; PRIOR APPLICATION NUMBER: PCT/EP00/08247

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PRIOR FILING DATE: 2000-08-24
  PRIOR APPLICATION NUMBER: EP 99116533
  PRIOR FILING DATE: 1999-08-24
  NUMBER OF SEQ ID NOS: 10
  SOFTWARE: PatentIn version 3.2
; SEO ID NO 9
   LENGTH: 4382
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   ORGANISM: Artificial Sequence
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US-09-906-158-10

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- ; Publication No. US20030078217A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Brett P. Monia
- ; APPLICANT: Susan M. Freier
- ; FILE REFERENCE: RTS-0257

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               (A) Nico Cerletti
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      NUMBER OF SEQUENCES: 13
      CORRESPONDENCE ADDRESS:
          ADDRESSEE: No. US20020115834Alartis Patent Department
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STREET: 564 Morris Avenue

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CITY: Summit
              STATE: New Jersey
              COUNTRY: USA
              ZIP: 07901
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              COMPUTER: IBM PC compatible
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              FILING DATE: 20-Mar-2001
         PRIOR APPLICATION DATA:
              APPLICATION NUMBER: PCT/EP95/02719
              FILING DATE: 12-Jul-95
              APPLICATION NUMBER: EPO 94810439.3
              FILING DATE: 25-Jul-94
         ATTORNEY/AGENT INFORMATION:
              NAME: Pfeiffer, Hesna J. .
              REGISTRATION NUMBER: 22640
              REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
         TELECOMMUNICATION INFORMATION:
              TELEPHONE: (908) 522-6940
              TELEFAX: (908) 522-6955
   INFORMATION FOR SEQ ID NO: 7:
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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(without alignments)

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 AUTHORS
           NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
  JOURNAL
            Unpublished
COMMENT
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
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             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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Db 6	TCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGAGC 739	
Qy 8	CCTGGATACCAACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTT 910	
Db 7	CCCTGGACACCAACTATTGCTT 761	
Qy 9	CAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCT 970	
Db 7	CAGCTCCCCGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAGGGACCT 821	
Qy 9	GGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTG 103	0
Db 8	CGGCTGGAAGTGGATCCACGAGCCCCAAGGCTACCATGCCCACTTCTGCCTCGGGCCCTG 881	
Qy 10	TCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCA 109	0
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Qy 11	ATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACAT 1198	
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RESULT 2 BX355682/c LOCUS DEFINITION	K355682 1201 bp mRNA linear EST 05-MAY-200 K355682 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA Lone CS0DI002YJ05 3-PRIME, mRNA sequence.	
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	(355682 (355682.1 GI:30371987 ST. Omo sapiens (human) Omo sapiens	
REFERENCE AUTHORS	ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 1201) 1,W.B., Gruber,C., Jessee,J. and Polayes,D.	

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TITLE
          Full-length cDNA libraries and normalization
 JOURNAL
          Unpublished
COMMENT
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 9160.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cqi?seq=CS0DI002CE03NP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0DI002CE03NP1.
FEATURES
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                  sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
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 Matches 904; Conservative
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                        Db
        928 GTTCAAGCAGAGTACACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGC 869
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        502 AAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCA 561
Qу
            808 AAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGGCGATACCTCA 749
Db
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            Db
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Qy	622	TTGTGCGGCAGTGCCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACT	681
Db	688	TTGTGCGGCAGTGGTTGAGCCCTGGAGGGGAAATTGA-GGCTTTCGCCTTAGCGCCCACT	630
Qy	682	GTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCC	741
Db	629	GCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCC	570
Qy	742	GCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCA	801
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Qy	802	CCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACCA	861
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Qy	862	ACGACTACAAGGATGACGACGACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGG	921
Db	453	ACCAACTATTGCTTCAGCTCCACGG	429
Qy	922	AGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGT	981
Db	428	AGAAGNACTGCTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGT	369
Qy	982	GGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCT	1041
Db	368	GGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTT	309
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Qу	1162	TGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCA	1221
Db	188	TGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCA	129
Qу	1222	GCTGAGGCCCGCCCCACAGCCCCGCCCACCCGGCCAGGCCCGCCCACCCCCGCC	1281
Db	128	GCTGAGGTCCCGCCCGCCCGCCCCGCCCCGCCCGCCCCGCCCCGCCCC	69
Qy	1282	CGCCTCACCGGGGCTGTATTTAAGGACATCGTGCCCCAAGCCCACTTGGGAT	1333
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clone CSODI013YH16 3-PRIME, mRNA sequence.
ACCESSION
          BX335351
VERSION
          BX335351.1 GI:30308367
KEYWORDS
          EST.
SOURCE
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 ORGANISM
          Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
             (bases 1 to 983)
REFERENCE
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 AUTHORS
          Full-length cDNA libraries and normalization
 TITLE
 JOURNAL
          Unpublished
COMMENT
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 9160.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seg=CS0DI013DD08NP1
          &cluster=9160.r. Contact : Feng Liang Email : fliang@lifetech.com
          URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0DI013DD08NP1.
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                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
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                  digested with Not I and cloned into the Not I and EcoR V
                  sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
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 Query Match
 Best Local Similarity
                       84.5%; Pred. No. 4.7e-143;
 Matches 859; Conservative
                           5; Mismatches 105; Indels
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        342 CGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCCAC 401
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            Db
        402 AGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTG 461
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            863 AGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTG 804
Db
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Db
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Db	743		684
Qy	582	AGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACC	641
Db	683	AGCGACTCGCCAGAGTGGTTATCTTTTGATGTCACCGGAGTTGTGCGGCAGTGGTTGAGC	624
Qу	642	CGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTGTTCCTGTGACAGCAAAGAT	701
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Qу	702	AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACC	761
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Qу	762	ATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAG	821
Db	504	ATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCCAG	445
Qу	822	CACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACCAACGACTACAAGGATGACGAC	881
Db	444	CATCTGCAAAGCTCCCGGCACCGCCGA	418
Qу	882	GACAAGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	941
Db	417	GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	364
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Qу	1002	TACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTAC	1061
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Qу	1182	GAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCCCCC	1241
Db	125	GAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGAGGTCCCGCCCCGCC-	67
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Db	66	CCGCCCCGCCCGGCAGGCCCGGCCCCACCCCGCCCCCGCCCCCGCTTG 15	

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DEFINITION BX349319 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
          Homo sapiens cDNA clone CS0DL010YL07 5-PRIME, mRNA sequence.
ACCESSION
          BX349319
VERSION
          BX349319.1 GI:30379410
KEYWORDS
          EST.
SOURCE
          Homo sapiens (human)
 ORGANISM
         Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
             (bases 1 to 900)
REFERENCE
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 AUTHORS
 TITLE
          Full-length cDNA libraries and normalization
 JOURNAL
          Unpublished
COMMENT
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 9160.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0BAG059ZD04_CS05596_1&cluster=9160.r.
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID: CS0BAG059ZD04 CS05596 1.
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                  25-NORMALIZED"
                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
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                  digested with Not I and cloned into the Not I and EcoR V
                  sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
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Qу
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QУ	310	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 369
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QУ	370	AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG 429
Db	390	AAATCTATGACAAGTTCAAGCAGAGTACACACACACATATATAT
Qу	430	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 489
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Qу	490	GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 549
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Db	570	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG 629
Qу	610	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC 669
Db	630	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC 689
Qy	670	TCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT 729
Db	690	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT 749
Qу	730	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC 789
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Qy	790	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG 849
Db	810	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGNCGAG 869
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RESULT 5 BX324511/c

1041 bp LOCUS BX324511 mRNA linear EST 02-MAY-2003 DEFINITION BX324511 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC024YD20 3-PRIME, mRNA sequence.

ACCESSION BX324511

VERSION BX324511.1 GI:30332381

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KEYWORDS
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SOURCE
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          Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             (bases 1 to 1041)
 AUTHORS
           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
          Full-length cDNA libraries and normalization
 JOURNAL
           Unpublished
COMMENT
           Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           Library was constructed by Life Technologies, a division of
           Invitrogen. This sequence belongs to sequence cluster 9160.r For
           more information about this cluster, see
          http://www.genoscope.cns.fr/
           cqi-bin/cluster.cqi?seq=CSOACO24DB10NP2&cluster=9160.r. Contact :
           Feng Liang Email : fliang@lifetech.com URL :
           http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
           Faraday Avenue Genoscope sequence ID: CSOACO24DB10NP2.
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                   /note="1st strand cDNA was primed with a NotI-oligo(dT)
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                   digested with Not I and cloned into the Not I and EcoR V
                   sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
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 Matches 870; Conservative 10; Mismatches 133; Indels
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         343 GCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCCACA 402
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Qy	642	CGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTGTTCCTGTGACAGCAAAGAT	701
Db	666		608
Qу	702	AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACC	761
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Qу	762	ATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAG	821
Db	547	ATTCATGGCATGAACCGGCCTTTCCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCCAG	488
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Db	487		452
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Db	451	ACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCG	407
Qy	942	CAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGC	1001
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Qy	1002	TACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTAC	1061
Db	346	TACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTAC	287
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Db	286	AGCAAGGTCCTGGCCCTGTACAACCAGCATAACCC-GGCGCCTCGGCGGCGCCGTG-TGC	229
Qy	1122	GTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTG	1181
Db	228	GTGCCGCAGGCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTG	169
Qy	1182	GAGCAGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCCCCC	1241
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Qy	1242	ACAGCCCCGCCCACCCGGCAGGCCCGGCCCCACCCCGCCTCACCGGG	1293
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DEFINITION BX434425 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE014YE16
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ACCESSION
           BX434425
VERSION
           BX434425.1 GI:30779291
KEYWORDS
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SOURCE
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           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
              (bases 1 to 888)
           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 AUTHORS
           Full-length cDNA libraries and normalization
  TITLE
  JOURNAL
           Unpublished
COMMENT
           Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           Library was constructed by Life Technologies, a division of
           Invitrogen. This sequence belongs to sequence cluster 9160.r For
           more information about this cluster, see
           http://www.genoscope.cns.fr/
           cqi-bin/cluster.cqi?seq=CS0BAK028AB08NM1&cluster=9160.r. Contact :
           Feng Liang Email : fliang@lifetech.com URL :
           http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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BASE COUNT
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Qy	732	AATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC	791
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ACCESSION
           BM555996
VERSION
           BM555996.1 GI:18796907
KEYWORDS
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SOURCE
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REFERENCE
              (bases 1 to 1043)
           NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
           National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM12261 row: i column: 16
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RESULT 8 BX383773/c

LOCUS BX383773 950 bp mRNA linear EST 08-MAY-2003 DEFINITION BX383773 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens

cDNA clone CS0DK001YA15 3-PRIME, mRNA sequence.

ACCESSION BX383773

VERSION BX383773.1 GI:30457168

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REFERENCE
             (bases 1 to 950)
 AUTHORS
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
           Full-length cDNA libraries and normalization
 JOURNAL
           Unpublished
COMMENT
           Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           Library was constructed by Life Technologies, a division of
           Invitrogen. This sequence belongs to sequence cluster 9160.r For
          more information about this cluster, see
           http://www.genoscope.cns.fr/
           cgi-bin/cluster.cgi?seq=CS0DK001AA08NP1&cluster=9160.r. Contact :
           Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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            (bases 1 to 859)
REFERENCE
 AUTHORS
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
          Full-length cDNA libraries and normalization
 TITLE
 JOURNAL
          Unpublished
COMMENT
          On Feb 13, 2001 this sequence version replaced gi:12793574.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen. This sequence belongs to sequence cluster
          9160.r For more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0DD009BG03QP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
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                  sites of the pCMVSPORT 6 vector. Library was normalized."
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cDNA clone CS0DD009YM06 5-PRIME, mRNA sequence.

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REFERENCE AUTHORS TITLE JOURNAL COMMENT		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 713) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D.

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Email: cgapbs-r@mail.nih.gov
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           cDNA Library Preparation: Ling Hong/Rubin Laboratory
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           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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                  California, Berkeley) using ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies).
                  Note: this is a NIH MGC Library."
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REFERENCE
            (bases 1 to 717)
 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
          National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
          Unpublished
COMMENT
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
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                in the laboratory of Gerald M. Rubin (University of
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                Note: this is a NIH MGC Library."
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REFERENCE
             (bases 1 to 902)
 AUTHORS
           NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished
 JOURNAL
           Contact: Robert Strausberg, Ph.D.
COMMENT
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
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                    by Ling Hong in the laboratory of Gerald M. Rubin
                    (University of California, Berkeley) using ZAP-cDNA
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REFERENCE
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 AUTHORS
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 JOURNAL
          Unpublished
COMMENT
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
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AUTHORS TITLE JOURNAL	Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished		

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          On Feb 13, 2001 this sequence version replaced qi:12793573.
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          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen. This sequence belongs to sequence cluster
          9160.r For more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0DD009BG03NP1&cluster=9160.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
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TITLE JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished						
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov						
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                  by Ling Hong in the laboratory of Gerald M. Rubin
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        565 ACCGGCTGCTGGCCCCCAGTGA--CTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGT 622
Qу
            1111111 111 1111 1111
                                    Dh
        715 ACCGGCTGGTGGCACCCAGCGAACTCGCCCAGAGTGGTTATCTTTTGATGTCACCGGAGT 656
        623 TGTGCGCCAGTGCCCGCAG-AGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACT 681
Qу
            Dh
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Qу
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Qy	1222	GCTGAGGCCCGCCCACAGCCCCGCCCACCCGGCCAGGCCCGGCCCACCCCCGCC	1281
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Search completed: October 28, 2003, 00:08:25 Job time : 3362.54 secs

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October 9, 2003, 15:56:23 ; Search time 5244 Seconds (without alignments) 10617.468 Million cell updates/sec
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1361
1 tggtaccgagatggcgcctt......cgattaaaqcggccgcgact 1361
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AK33103 Sus scrofa AK3313 Porcine mRN Y00111 Porcine mRN AF46108 Sus scrof L34956 Canine tran B00973 cDNA encodi A06669 Synthetic m X76916 O.aries mRN BC000125 Homo sapi BC001180 Homo sapi BC001180 Homo sapi BC00125 Squence 2 X02812 Human mRNA 108268 Squence 3 I08275 Sequence AX615128 Squence AX615128 Sequence AX615128 Sequence AX615128 Sequence AX615128 Sequence AX528619 Sequence AX528619 Sequence AX528619 Sequence AX528619 Sequence AX528619 Sequence AX528619 Sequence AX53664 Sequence AX53664 Sequence I05434 Sequence I03312 Sequence I03312 Sequence I03312 Sequence I03312 Sequence AX455100 Sequence I03312 Sequence AX455100 Sequence	mRNA linear MAM 31-MAR-1995 or beta-l mRNA, complete cds. ata; Vertebrata; Euleleostomi; ; Suina; Suidae; Sus. g,E., Ludwig,R.L., Dhar,R., g growth factor-beta l mRNAs.
Q.	AX3316 AX3316 AX3316 GGTGFB1 SSTGFBR E00973 AZ40659 AA7GFB1 BC001180 AA7GFB1 BC001180 AA7GFB1 BC00125 BC001180 AA7GFB1 BC00125 BC001180 AA7GFB1 I0826 HGTGFB1 I08275 BT007866 BC0222 AX615127 AX61432 AX615127 AX615127 AX615127 BC01373 AX615127 BC013738 AX615128 AX528615 I03310 AX528615 I03310 AX528615 AX528615 AX528615 AX528615 AX528615 AX528615 AX528615 I03312 AX528615 AX528616 AX336646 IUMATCFB4 AX336646 IUMATCFB4 AX336646 IUMATCFB4 AX55100 MA765110 AX455100 MA76FB1 CHKTGFB4	3206 bp ing growth fact factor-beta-1. thordata; Crani tetartiodactyla srghen-Schillin s,A.B.
Length DB	3306 173266 173366 173367 173368 17337	ゅ てらさ したりとらっ
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09-JAN-2002
                                                                                                                             1681 TCCTCATGGCCACCCCGCTGGAGAGGCCCAGCACCTGCACAGCTCCCGGCACCGCGGA- 1739
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Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1870 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
                                                              786 TCCTCATGGCCACCCGCTGGAGAGGCCCAGCACCTGCACCAGCTCCGGCACCGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                              -----GCCCTGGATA
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                1381 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                          1026 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
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                                                                                                                                                                                            726 TCAATTCTGGCCGCCGCGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC
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                                                                                                            606 ATGICACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC
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Sequence 1 from Patent WO0181404.
AX338213
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RIEARROGILSKLRANSPSGODVPPGEPLEAVLALKINSTRORVAGESVEPEPEBAD
YYAKEYTRUAWYESONOLYDKFKGTPHSLYMLFWTSELERAYPEPVLLSRAELRLIK
KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
RAAHGSCDSTEKNCVRQLAITHORNSRERADATHTMENRPAIESRH
RRALDTNYGFSSTEKNGVRQLAITHORNSLAFKDLANTPLESAQHHHSRH
OYSKVLALYNQVRQLYIDFRKDLANTPLESAQHHHSRH
OYSKVLALYNQVRGRAAAPCCVPQALEPLPIVYYVGRRPKVEQLSNMIVRSCKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTCAAGTTAAAAGTGGAGCAGCTGGAGCTATACCAGAAATACAGCAATGATTCCT 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
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                                                           On Apr 1, 1995 this sequence version replaced gi:341017.
Original source text: Sus scrofa (strain miniature swine) cDNA
mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC
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1201 CAACATGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCCACAGCCCCGCC 1260
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Jakowlew,S.B., Dillard,P.J., Sporn,M.B. and Roberts,A.B.
Nucleotide sequence of chicken transforming growth factor-beta 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-JUL-1988) Jakowlew S.B., National Institute of health, National Cancer Institute, Laboratory of Chemoprevention, Building 41, Room B902, Bethesda, Maryland 20892, USA The submitters believe that the chicken cDNA library was contaminated with porcine cDNA, and that the sequence is infact
                                                                                                                                                                                                      CACCCGGCAGGCCCGGCCCCACCCCCCCCCCCCCCCGGGGCTGTATTTAAGGACATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1214 CACCCGGCAGGCCCGGCCCCACCCCCCCCCCCCCCCGGGGCTGTATTAAGGACATCG
CCTGCTCCTCATGGCCACCCCGCTGGAGAGGCCCCAGCACCTGCACAGCTCCCGGCACCG
                                                                                               GCTGGAGCCACTGCCCATCGTGTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTC
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                          CGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCCATGAACCGGCCCTT
                                                                                                                                                                                                                                                                                                                                                                       GGTGFB1 1750 bp mRNA linear Porcine mRNA for transforming growth factor-beta 1. X12373
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Lransforming growth factor-beta 1.
Sus scrofa (pig)
Sus scrofa
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Jakowlew, S.B.
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/codon_start=1
/protein_id="Cab20538.1"
/protein_id="Cab20538.1"
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KLKVEGNYELYQYX SNDSNRYLARSISSEMLASPDTGVYVYROWLTRREAIGEFR
ISAHSSSDSKDNYLHYEINGFRSGRREDLATIHGMRRPFLLLMATPLERRAHLESKH
RRALDTNYCFSSTEKNCVRQLYIDFREDLATHGMRRPFLLLMATPLERRACHTHSSKH
RRALDTNYCFSSTEKNCVRQLYIDFREDLATHGMRRPFLLLMATPLERRACHTHSSCH
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Inducible plasmid vector encoding tgf.-g(b) and uses thereof patent: WO 101404-A 1 01-NNOV-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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Pred. No. 1.3e-209;
0; Mismatches 7; Indels 53;
                                                             /organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
16. 1188
                                        Location/Qualifiers
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ilarity 95.6%;
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                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 1605)
Derynck, R. and Rhee, L. Sequence of the porcine transforming growth factor-b Nucleic Acids Res. 15 (7), 3187 (1987)
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transforming growth factor-beta
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TQYSKVLALYNOHNPGASAAPCCVPQALEPLFIVYYVGRKPKVFQLSNMIVRSCKCS"
1285. 1619
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1620. 1750
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KLKVEQHVELYQK%SNDSWGYLSNRLLAPSDSPEWLSFDVTGVVRQWLIRREAIEGFR
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Pred. No. 8e-208;
0; Mismatches 1
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                                      /organism-"Sus scrofa"
/mol_type-"mRNA"
/strain-"whita leghorn"
/db_xref="taxon:9823"
/clone-"pTGFB-chx119"
/cell_type-"chondrocyte"
1. 1750
/gene-"TGF-beta 1"
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Location/Qualifiers
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/gene="TGF-bet:a 1"
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/gene="TGF-beta 1"
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Best Local Similarity 94.8%;
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AF461808 2221 bp mRNA linear MAM 03-JAN-2002 Sus scrofa transforming growth factor beta 1 (TGFB1) mRNA, complete
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                         606 ATGICACCGGAGITGIGGGGGAGIGGCIGACCCGCAGAGAGGCIAIAGAGGGTIIICGCC
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Wimmers,K., Chomdej,S., Ponsuksili,S. and Schellander,K.
Direct Submission
Submitted (20-DEC-2001) Institute of Animal Breeding Science,
University of Bonn, Endenicher Allee 15, Bonn 53115, Germany
Location/Qualifiers
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Wimmers.K., Chomdej,S., Ponsuksili,S. and Schellander,R.
Polymorphism in the porcine transforming growth factor.
Unpublished
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LSAHCSCDSKDNTLHVEINGFNSGRRCDLATHGMNRPFLLLMATPLERAOHLHSSRH
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1238. .1573
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572 c 437 g 298 t
                                                  /organism-"Sus scrofa"
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GGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTAC 1090
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Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete
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L34956.1 GI:516071
homologue, transforming growth factor-beta 1.
Canis familiaris (dog)
Canis familiaris
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0; Mismatches 8; Indels
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                                                          /note-"cytokine"
chromosome="6"
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                                           /gene="TGFB1"
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Best Local Similarity 95.2%;
Matches 1176; Conservative
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PD 29-SEP-1986;
PP 20-MAR-1986 JP 1986064661
PP 20-MAR-1985 US 8B 715142
PI RIKU MAIKERU ANDORE DENTRODO BANNOOMAN GETSUDERU PC C12P21/00,C12N1/00,C12N15/00/C12N15/00/C12N15/00,PC C2 strandedness: Double;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[1] (bases 1 to 2527)
[8] Riku, M.A.D.D and Debitsudo, B.G.

NUCLEIC ACID CODED WITH TGF-BETA AND ITS USE
NUCLEIC ACID CODED WITH TGF-BETA AND ITS USE
Patent: JP 1986219395-A 1 29-SEP-1986;

CS human

PN JP 1986219395-A/1

PD 29-SEP-1986

PP 20-MAR-1986 US 85 715142

PP 22-MAR-1986 US 85 715142

PI RIKU MAIKERU ANDORE DERINKU, DEBITSUDO BANNOOMAN GETSUDERU PC
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                                     773 TCAGTTCCAGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGACCTTCCTGC 832
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Homo sapiens
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/prodein_id="AaA51458.1"
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/db_xref="d1:516072"
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RRALDDNYCFSSFSCROCVPGLATDFRCHAFFT
OYSKYLALYNGHNPGASAARCCVPQALEPLPIVYTVGRKPRVFGLSNMIVRSCKCS"
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1231. 1369
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/gene-"TGFB1"
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/product-'pre TGF-beta'

1676. .2011

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Acrganism="Hono sapiens"
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MAM 18-APR-1995
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
GGCAGGCCCGGCCCCACCCCGCCCGCCT-----CACCGGGCTGTATTTAAGGACA
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                                                    GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
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Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept..
Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
Edinburgh EH9 IQH, UK
Location/Qualifiers
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    /codon_start=1
    /product_transforming growth factor-beta
/protein_id="CAR54142.1"
    /db_xref="GI:496649"

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Sequence and chromosomal localisation of
latent transforming growth factor-beta 1
Gene 150 (2), 371-373 (1994)
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/mol_type="mRNA"
/db_xref="taxon:9940"
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Bovidae; Caprinae; Ovis.
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                                                                                                                       CCCCCATGCCGCCTCCGG3CTGCGGCTGCTGCTGCTGCTACCGCTGCTGCTGCTGCTAC
                                                                                                                                                                                          Gaps
                                                                                              59;
                                                                  Length 2537
                                                                                              Indels
                                                                Score 978.8; DB 6;
Pred. No. 1.9e-167;
0; Mismatches 147;
                                                                  Query Match 71.9%;
Best Local Similarity 84.8%;
Matches 1146; Conservative
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Contact: MGC help desk ktp://mgc.nci.nih.gov
Iissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Proparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lec, Victor Ling, Carrie Mathowson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Nalasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens, Similar to transforming growth factor, beta 1, clone MGC:3319 IMAGE:3351664, mRNA, complete cds. BC000125 BC000125.1 GI:12652748 MGC.
                                                                                                                                                        GGGCCCTGTCCCTACAICTGGAGCCTAGACACTCAGYACAGCAAGGTCCTGGCTCTGTAC 1090
  Bukaryota; Metazoa; Chordata: Craniata: Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1780)

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Submitted (03-NOV-2000) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: e Column: 11 Ilis clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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./tissue_type="gyp" ret;
./clone_lib="NIB_MGC_l6"
/lab_host="DH10B-R"
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/mol_type="mRNA"
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                                                                                                                  Gaps
                                                                                                                51;
                                                                              Length 1173;
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/product="transforming growth factor-beta
378 c 336 q 214 t
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                                                                              DB 4;
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Pred. No. 2.5e-166;
(; Mismatches 87;
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Best Local Similarity 88.7%;
Matches 1086; Conservative
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (11-2EC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genemics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                   TTCTCATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGGTCCCGGCACGCCGGA-
                                                                                                                    TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCCACAGCCCCGCCCACACC
                                CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA
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                                                                                                  CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGGCGCAGCTCTACATTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
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Tissue Procurement: ATCC
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BC001180.1 GI:12654682
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KIKYEQHYELYQXXSNNSWRXLSNRLAPSDSPEMLSSDVTGVVROWLSRGEIEGFR
ILSAHGSCDSRDWTLQYDINGTTGRRGDLATHGWRRPFLLLMATPLERAGHLGSSRH
RRALDTNYCFSSTEKNGCVRQLYIDFRKDLGWRWIHEPRGYHANFCLGPCPYIWSLDT
QYSRVLLALYNOHNDGARAPCGVPQALEPLPIVYYVGRRFKVFGLSNMIVRSCKGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                606 ATGTCACCGGAGTTGTGCGCCAGTGGCTGACCCGCAGAGGCTATAGAGGGTTTTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGTGCCCACTCTTCCTCTGACAGGAAAGATAACACACTCCACGTGGAAATTAACGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCATGGCCACCCCGCTGGAGGGCCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG
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                                                                                                                                                                                                                                                 Score 972.4; DB 9; Length 1780;
Pred. No. 2.8e-166;
3; Mismatches 151; Indels 59;
                                                                                                                                                                                                                                                      71.48;
                                                                                                                                                                                                                                                                                      Matches 1142; Conservative
                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                           AGMTGFB
Simian transforming growth factor-beta (TGF) mRNA, complete cds. M16658
M16658
M16658
Growth factor; transforming growth factor-beta.
Gercopithecus aethiops (African green monkey)
Gercopithecus aethiops
Gercopithecus aeth
                               TGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1471 IGTACAACCAGCATAAACCCGGGGGCGCGCGGCGCGTGCTGCTGCTGCTGCTGGCGCGCGTGG
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     GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG
                                                                                                    ATGICACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC
                                                                                                                                                                                                      TCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT
                                                                                                                                                                                                                                                                                                     TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC
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1 (bases 1 to 1561)
Sabsples, K., Plowman, G.D., Rose, T.M., Iwardzik, D.R. and Purchio, A.F.
Cloning and sequence analysis of simian transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
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/product="imilar to transforming growth factor, beta 1"
/protein_id="AaM011801"
/d=xref="i12654683"
/translation="wPPSGERLLLLLPLLMLLVLTPERPAACLSTCKTIDMELVKRK
RIEARRGOLLSKLRASPPSGCEVPROFPLPRWTSELREAPEPPLLSRAEHELRL
RYAKUPYRVLMFTHNET!VERKOSTHSIVMFFWTPSELREAPEPPLSRAEHELRL
KLKVEGHYELYOKTSNNSWFYLSNRLAPSDSPEWLSFDYTGVRQWLSRGEIEGFF
LSAHCSCDSRONTLQVDINGFTTGRRGDLATHGMNRPFLLLMATPLERAQHLQSSRH
RRALDTNTGFSSTEKNCYNGVITDFRXDLGWWHIPERGYHNFCLGPCPYIWSLDT
GYSKVLALYNGHNPGASAAPCCVPQALEPLPIVYYVGRKRVVBQLSNMIVRSCKCS"
648 c 493 g 298 t
                                                                            found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
                                                                       Clone distribution: MCC clone distribution information can be for through the I.M.A.G.E. Consortium/KLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Wow: e Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 37097.
     Jill Vardy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC
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Michael Thorne, Miranada Tsai, Natasja van den Bosch,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                 1...1780
/organism="Hcmo sapiens"
/mol_type="mkNa"
/db_xxef="taxon:9606"
/clone="MGC:2323 IMAGE:335605"
/tlosue="type="fye, retinoblastoma"
/clone=lbb="knH_MGC_16"
/lab_host="bH10B-R"
/note="Vector: poTB7"
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.4%;
Best Local Similarity 84.5%;
Matches 1142; Conservative 0
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                                   TCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT
                                                                                                              TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC
                 ATCTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGGTTTTCGCC
                                                                                                                                                                                                                                                                                                                  CCCTGGATACCAACAGCTACCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1821)
Ohashi,H., Ishii,Y., Miyata,Y., Miyazono,K., Miyagawa,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRODUCTION OF HUMAN PRO-TGF-BETA1 BY GENETIC RECOMBINATION PALENT: JP 1991180192-A 1 06-AUG-1991; KIRIN BREWERY CO LTD OS HUMO SAPIORS (human) PN JP 1991180192-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1318 -TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
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Homo sapiens
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                                                                          MIYAGAWA KIYOSHI, TAKAKU FUMIMARO
CI2P21/00,C07K13/00,C12N5/10,C12N15/18//C12Q1/68,(C12P21/00,
C12R1:91),
(C12R15/18,C12R1:91);
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511. .1683
/product='human prepro TGF-betal'
06-AUG-1991
07-DEC-1989 JP 1589318243
OHASHI HIDEYA, ISHII YASUYOKI, MIYATA YOSHINORI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3core 968.2; DB 6; Length ]
2red. No. 1.6e-165;
0: Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                       . 597
598. .1680
/note-'human pro TGF-betal'
1345. .1680
/product-'human TGF-betal'
1584. .1820.
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                       *source: tissue_type=placenta; *source: clone=pVC19-TGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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hypothetical: No;
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71.1%;
Best Local Similarity 84.9%;
Matches 1133; Conservative
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C12R1:91/
PC C12R1:92
CC Strander
CC topology
CC hypother
CC *Source:
FH Key
FT 5'UTR
FT CDS
FT 5'UTR
FT CDS
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                                 1085 TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC
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                                                                                                                                                                             1025 TTAGGGGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT
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                AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG
                                                                                                                        785 AGCICCGAGAAGCGGIACCIGAACCCGIGIIGCICICCCGGGCAGAGCIGCGICTGAA
                                                                                                                                                           GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT
                                                                                                                                                                                                                             546 GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG
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/product="Union" (protein for MGC:22008)"
/protein_id="AAH2242.1"
/d_xref="C1:18490116"
/dxxef="C1:18490116"
/translation-"HPPSGGEVPFGPLPEAVLALYNSTRDRVAGESAEPEPEAD
XTARAVTROLMSTHNETYDFKGGTHSIYMFFNTSELREAPEPPULSAELELER
KLKYEGHYELYQXTSHNSWFLSRRLAPSDSPEWLSFDYTGVRQMLSRGGEIEGFR
LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHIQSSRH
RRALDTNYCFSSTERNCVRQLYIDFRDLGWWHIPPRGYHANFCLGDCPYIWSLDT
QYSKVLALYNGANARAPCCVRQLYIDFRDLGWWHIPPRGYHANFCLGDCPYIWSLDT
QYSKVLALYNGANARAPCCVRQLYIDFRDLGWWHIPPRGYHANFCLGDCPYIWSLDT
07 SYSVLALYNGANARAPCCVRQLYIDFRDLGWWHIPPRGYHANFCLGDCPYIWSLDT
07 SYSVLALYNGANARAPCCVRQLYIDFRDLGWWHIPPRGYHANFCRGSCRGS"
                               WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: AfCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
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                                                                                                                                                                                                               Myers,
                                                                                                                                                                                                                                                               Clone distribution: M3C clone distribution information can be for through the I.M.A.G.E. Consortium/Linn.at: http://image.llnl.gov Series: IRAK Plate: 27 Row: e Column: 21 This clone was selectied for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
Room 11A03, Bethesda, MD 20892-2590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGAGAIGGCGCCTTCGGGGGCTCTTGCCGCTGCTGCTGCCGCTGTGGCTGC
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Dickson, M., Schmutz, J., Grlmwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo saplens"
/mol_type="mRNA"
/dol_rxfe='taxon:9606"
/clone="MGC:22008 INAGE:4399762"
/tissue_type="buodenum, adenocarcinoma"
/clone_lib="VIH_MGC_88"
/lab_host="billo8"
/note="Vector: pCMV-SPORT6"
370. 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 967.8; DB 9;
Pred. No. 1.9e-165;
); Mismatches 147;
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1. .1746
 31 Center Drive,
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Purchlo.A.F., Gentry,L. and Twardzik,D.
Cloning and expression of simian transforming growth factor-SSI
Patent: EP 0293785-A2 2 07-DEC-1988;
Location/Qualifiers
                                                                                                                                                                                                                CGGGAAGCGGTGCCGGAACCTGTAITGCTCTCGGGCAGAGCTGCGGCCTGCTGAGGCTC
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Pred. No. 3.3e-165;
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Sequence 2 from Patent
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106216.1 GI:590649
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ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCGGAGCCCTG
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Simian transformin

Human pro-TCF-beta Coding sequence of Simian Transformin

Sequence encoding

Monkey transformin TGFbetal 5'-UTR-CD

Human transforming

cDNA encoding tran Nucleotide sequenc

AAH28216

Coding sequence of Human Transforming

AAQ29177 AAQ29177 ABV75391

AAQ03509

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Androgen receptor
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(without alignments)
8563.951 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence encoding
TGF-beta 1.Deta 2
TGFB1 Arg25frc pol
Human TGF beta 1 p
Human TGF beta 1 b
Human TGF beta 1 D
Human polynucleot1
TGF-beta 1. Homo
Human polynucleot1
TGF-beta 1. Homo
Human polynucleot1
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DNA encoding LAP-h
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Hybrid transformin
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Simian-human hybri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "Porcine TGF-betal mutant protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porcine transforming growth factor beta 1 (TGF-betal) cDNA.
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                                                    ABX0981
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(USSH) US DEPT HEALTH & HUMAN SERVICES.

20-APR-2000; 2000US-199014P.

Sequence encoding CDNA encoding huma Sequence of pre-TG Pre-Transforming 9 Human pre-TGF-beta Human pre-transfor

AAQ03301 AAQ02814 AAT15720 AAQ56923 AAV52933

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Androgen receptor; transactivation; modulator; Smad3; Smad4; Akt; TGF-B;
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                                                                                                            CCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACGG
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             CGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTT
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TTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTC
                                                      CTTTGATG1 CACCGGAGTTGTGCGGCAGTGGCTGACCGGCAGAGAGGCTATAGAGGGTTT
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                                                                                                                                                                The invention relates to a composition containing a vector comprising a gene encoding a regulatory transcription factor under the control of a promoter encoding a transforming growth factor-beta (TGF-beta). The promoter encoding a transforming growth factor-beta (TGF-beta). The vector is useful for expressing TGF-beta, such as TGF-beta). TGF-beta.

Or TGF-beta3, its variants or homologues, by transfecting a cell which is part of a host suspected of having an autoimmune disease, especially inflammatory bowel disease (TBD), under conditions such that the collypeptide encoded by the nucleic acid sequence in the vector is callivery of the vector is delivery system. The delivery of the vector results in substantial elimination of symptoms of the autoimmune disease and increased production of IL-10 by the host. The composition is useful for treating various diseases with an autoimmune composition is useful for treating various diseases with an autoimmune composition is useful for assaying the expression of a gene in a cell. The vector is further useful for assaying the expression of a gene in a cell. The vector is further useful for screening of the effect of test compounds on cytokine (e.g. TGF-beta) expression of transfected cells.

The present sequence is a cDNN encoding porcine TGF-betal mutant.
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                                                                                Composition for treating autoimmune diseases e.g. inflammatory bowel disease in humans, comprises vector containing transforming growth factor-beta under the control of inducible promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other;
               Fuss
             Kitani A,
                                                                                                                                          Claim 1; Fig 1; 78pp; English
            Strober W, Nakamura K,
                                       WPI; 2002-026155/03.
                                                        P-PSDB; AAE13596
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                                                                                                                                                                                                                                                                         activity or androgen receptor-mediated transactivation activity in action cell. The method involves administering a compound which causes modulation of the androgen receptors activity and the inhibition of interaction between the receptor and a protein involved in a signal transduction pathway. The compound also inhibits the interaction between the androgen receptor and a protein selected from Smad3, Smad4, Akt, transforming growth factor (IGF)-B and phosphatase and tensin homologues deleted on chromosome 10 (PTEN) or their fragments. The compounds of the invention have cytostatic and antiproliferative activity. The obtained composition is useful for treating any disease, where uncontrolled proliferation or cellular proliferation occurs such as cancer, e.g. prostate cancer. This sequence represents the androgen receptor transactivation signalling pathway modulator E00973 described in the method of the invention.
                                                                                                                                                                                                                                                                invention describes a novel method for modulating androgen receptor
                                                                                                                                                                                Modulating androgen receptor activity, by administering a compound that modulates receptor activity, inhibits receptor-signal transduction pathway/receptor-coactivator interaction or changes amount or receptor
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Pred. No. 2.3e-188;
C; Mismatches 149; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2527 BP; 472 A; 888 C; 735 G; 432 T; 0 other;
                                                                                                                                                                                                                                          Disclosure; Page 225-226; 302pp; English.
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                                                                            2001US-282266P
                                                        2002WO-US11086
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Matches 1142; Conservative
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                                                                                                                                                            WPI; 2003-046871/04
          WO200282081-A2
                                                                            06-APR-2001;
13-MAR-2002;
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GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
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                                       486 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT
                                                       1437 AIGTCACCGGAGTIGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCC
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                                                                                               546 GGGGCTACCICAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCTTTG
                                                                                                                                                       TCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGT
                                                                                                                                                                   CAACCCCACTTGGGATCGATTAAA 1349
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GGCAGGCCCGGCCCCACCCCCGCCCCCCT-----CACCGGGCTGTATTTAAGGACA 1317
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                                                               AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG
                                                                                           GGCTCAAGITAAAAGIGGAGCAGCAGGIGGAGCIATACCAGAAATACAGCAAIGATICCI
                                                                                                                                     GGCGCTACCTCAGCAACCGGCTGCTCGCCCCCAGTGACTCACCGGAGTGGCTGTCTTTG
                                                                                                                                                                              606 ATGTCACCGCAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC
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                                                    AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCCGGGCAGAGCTGCGCCTGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The gene product is known to stimulate cell proliferation and inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in theatment of burns and the promotion of surface and internal wound healing. TGF-beta may be expressed from a (updated on 31-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                   TGF-beta prodn. from transformed hosts - useful esp. for treating wounds (J6 2/9/86).
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                                                                                                      stable hairpin loops'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.9%; Score 978.8; DB 7; Length 2537; Best Local Similarity 84.8%; Pred. No. 3.4e-188; Matches 1146; Conservative 0; Mismatches 147; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                              Transforming growth factor beta; cancer; wound healing
                                                                                                        form
                                                                                                        can
                                                                       Location/Qualifiers 37..113 /*tag= a /note= "Sequence can
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1b; 26pp; English
          Sequence encoding prefGF-beta.
                                                                                                                                                                                                                                  85US-0715142
87US-0025423
                                                                                                                                                                                                             86EP-0302112
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/*tag~ b
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                                                                                 misc_structure
                                                                                                                                                                                                                                  22-MAR-1985;
13-MAR-1987;
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                                                                                                                                                                                                                                                                                      Derynck RMA;
                                                    Unidentified
                                                                                                                                      mat_peptide
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                                                         TTGCCAGCCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG
                                                                          246 CICTITACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC
                                                                                                                                 AAATCTATGATAAATTCAAGGGCACCCCCCCACAGCTTATATATGCTGTTCAACACGTCGG
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AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC
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                                                                                       cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGAGATGCCCCCTTCGGGGCTGTGCCCCTTGCCGCTGCTGCTGCCGCTGTGGCTGC
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cloned into expression vectors for expression in eukaryotic host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 978.8; DB 11; Length 2537;
Pred. No. 3.4e-188;
3; Mismatches 147; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                     /note="G-C rich sequence
and a downstream TATA-like sequence"
                                                                                                                               Transforming growth factor-beta-1 (TGF-beta-1);
neoplastic cell line inhibition;
EGF-potentiated anchorage-independent growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                      /*tag= c
/note="stable hairpin loops"
2015..2100
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                                                                                                                                                                                                                       Location/Qualifiers
842..2014
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37..113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
71.9%;
Best Local Similarity 84.8%;
Matches 1146; Conservative
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cells for therapeutic use
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                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                              Homo sapiens
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                                           25-MAR-2003
05-AUG-1990
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               AAQ03301;
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TCF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic acid encoding the second subtype of TGF-beta (IGF-beta 3) is useful as a probe or to produce TGF-beta 3 for inhibition of growth of normal and uneoplastic cells.

(Updated on 31-CAT-2002 to add missing OS field.)

(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA
                                                                                                                                                                                                                                                                                                                  66 TAGTGCTGACGCCTGGCCGGCCGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  726 TCANITCTGGCCGCCGCGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACAGGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             606 ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGGCCTATAGAGGGTTTTCGCC
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                                                                                                                                                                                                                                                  246 CICITIACAACAGIACCCGCGACCGGGTAGCCGGGGAAGIGTCGAACCGGAGCCCGAGC
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                                                                                                                                                                                  Query Match 71.9%; Score 978.8; DB 11; Length 2537; Best Local Similarity 84.8%; Pred. No. 3.4e-188; Matches 1146; Conservative 0; Mismatches 147; Indels 59;
                                                                                                                                                    Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
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     GGCAGGCCCGGCCCCACCCCGCCCGCCT - - - - CACCGGGGCTGTATTTAAGGACA 1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence encodes the 390 amino acid (AA) precursor transforming growth factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of potential secondary structure. The TATA-like sequence in the 3' untranslated region of the gene is presumably a polyadenylation signal. Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3, for growth inhibition of certain normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
                                                                                                                                     CCGTGCCCCAAGCCCACCTGGGGCCCCATTAA 2137
                                                                                                                   TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
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842..2011
/#tag- a
/|aba|-pre-TGF beta 1
1677..2011
/#tag- b
/|aba|-mature TGF-beta 1
2015..2092
/#tag- c
2093..2099
/*tag- d
/*tag- d
/|aba|-TATA-like sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig. 1b; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                               Sequence of pre-TGF-betal cDNA
                                                                                                                                                                                                                                AAQ02814 standard; cDNA; 2537
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P-PSDB; AAR04034.
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WPI; 1996-076891/08.
P-PSDB; AAR90827.
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22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
                                                                                                                     05-NOV-1993;
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                                     polyA_signa
                                                  misc_signal
       TATA_signal
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                                           TCCGGAAGGACCTGGGCTGCAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1025
                                                  GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085
                                                                                                     1926 AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1985
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                                                                                                                                                                                               GGCAGGCCCGGCCCCCCCCCCCCGCCT-----CACCGGGGCTGTATTAAGGACA 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "GC-rich region forms stable hairpin loops; similar to structural organisation of c-myc RNA, could play role in mRNA stability or in regulation of transcription"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "GC-rich region; possibly responsible for the fact 3'UTR of mRNA could not be cloned as CDNA: may be important for transcription efficiency"
             CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGGCGGCGGCTCTACATTGACT
                                                                                                                                                                                                                                                                                                                                                         transforming growth factor beta 1; wound healing; recombinant production; ss.
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2015..2100
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/product= p
1676..2011
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/*tag= a
37..113
/*tag= b
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25-JAN-1980
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1137 CTGAGGCCGATACTACGCCAAGGAGGTCACCGCGTGCTAATGGTGGAAACCCAAAGG 1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The cDNA encodes the pre-transforming growth factor (TCF) beta 1 protein. The nucleotide sequence was obtd. by an analysis of several overlapping cDNAs and gene fragments. The DNA is useful for the recombinant production of TGF beta 1, which can be used in, e.g. wound healing. (Revised entry submitted to correct sequence analysis breakdown.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant human transforming growth factor-beta prods. - produced using Chinese hamster ovary cells, for use in diagnostic applications or in therapy
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/*tag= f
2094.:2100
/*tag= g
/note= "TATA-like sequence; no evidence that this
functions a promoter"
2514.:2520
/*tag= h
2599.:236
/*tag= "consensus sequence immediately precedes
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                                                                                                                                                                                                                    "consensus sequence immediately precedes
polyA-tail (Benoist et al)"
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85US-0715142.
89US-0389929.
92US-0845893.
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     AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG
                                                                          546 GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG
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                            AGCICCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCGGGCAGAGCTGCGCCTGCTGA
                                                   GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT
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AA056923 standard; cDNA; 2537 BP

RESULT 7 AAQ56923 ID AAQ5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925) and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.8%; Score 977.2; DB 15; Length 2537; Best Local Similarity 84.7%; Pred. No. 7.1e-188; Matches 1145; Conservative 0; Mismatches 148; Indels 59;
                                                                                                       TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing; vulnerary; ss.
                                                                                                                                                                                                                                                                         Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic probes, and for use in therapeutics
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                                                                                                                                                                                                                                     Location/Qualifiers
47..113
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87US-0025423.
89US-0389929.
92US-0845893.
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  (updated)
(first entry)
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                                                               Human pre-TGF-beta-1.
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P-PSDB; AAR46227.
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13-MAR-1987;
04-AUG-1989;
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25-MAR-2003
09-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag- b
/note= "putative stable hairpin loop"
2015..2100
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                                                                                                                       2106 CCGTGCCCCAGCCCACTGGGGCCCCATTAA 2137
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/note= "GC-rich sequence"
2514..2520
/*tag= d
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842..2014
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95US-0454468
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1676..2011
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P-PSDB; AAW78785.
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21-DEC-1998
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       83
Transforming growth factor-beta 1; TGF-beta 1; human;
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Transforming growth factor-beta; psoriasis; TGF-beta;
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12-AUG-1990
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                                                                                                                                      Gaps
TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of neoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications. TGF-beta nucleic acids are clopeated on 25-MAR-2003 to correct PF field.)
                                                                                                                                     265
                                                                                                                                     Indels
                                                                                                                  Length
                                                                                               Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;
                                                                                                                                     0; Mismatches 150;
                                                                                                                 Score 974; DB 19;
Fred. No. 3.1e-187;
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Best Local Similarity 84.5%;
Matches 1143; Conservative
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GGCAGGCCCGGCCCCACCCCCCCCCCCCCCT-----CACCGGGGCTGTATTAAGGACA 1317
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                                                          peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Headmostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; gene therapy;
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2000US-0662191.
2000US-0693036.
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                   Gaps
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           compositions
                                                                                                                                                            Length 1561;
                                                                 TGF-beta may be used in the treatment of hyperplasia associated with acanthosis-categorised skin diseases, and in alleviating psoriatic symptoms associated with cytokine-induced phenomen. See also AAQ03269 and AAR03750. (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                        Score 971; DB 11; Length 1
Pred. No. 1.2e-186;
0; Mismatches 145; Indels
                                                                                                                                    Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with containing transforming grow—h factor-beta.
                                             Disclosure; fig 1; 20pp; English
                                                                                                                                                          Query Match 71.3%;
Best Local Similarity 84.8%;
Matches 1148; Conservative
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                                            ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC
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                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM4213) with nootropic, the encoded polypeptides (AAM3642-AAM4213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system and as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system disease, such as latentar a scherosis, and Shy Darger Syndome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and consistent the sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 GGCTCAAGTTAAAAGTGGAGCAGCTGTGGAGCTGTACCAGAAATACAGCAACAATTCCT 1376
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                Wang
                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
              Ren F, W
Zhang J;
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            Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2742 BP; 526 A; 938 C; 799 G; 479 T; 0 other;
            Tang YT, Liu C, Asundi V, Chen R, Ma Y, '
Wang J, Wang Z, Wehrman T, Xu C, Xue AJ,
Zhao QA, Zhou P, Goodrich F, Drmanac RT;
                                                                                                                                                              Claim 1; SEQ ID NO 545; 10078pp; English
                                                                    WPI; 2001-442253/47.
P-PSDB; AAM39186.
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                GCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTCAAT
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                                                     AAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC
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                                                                                                                                                                                                                                                                                                                         Use of transforming growth factor (TGF)-beta and their antagonists – for modulating blood pressure, for treating hypertension and hypotension
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Pred. No. 3.6e-186;
0; Mismatches 144;
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Best Local Similarity 84.9'
Matches 1144; Conservative
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P-PSDB; AAR20124.
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                        426 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity 84.9%; Pred. No. 4.5e-186;
Matches 1133; Conservative 0; Mismatches 143; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA sequence encodes human prepro-TGF-beta 1 which can be
                                                                                                                                                                                                                                                                                                                                                                                   Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by preparing DNA chain contg. base sequence coding for human pre:pro-TGF-beta 1, forming expression vector etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant methods, it has osteogenetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;
                                                                                                                                              /*tag c
/note= "pro-TGF-beta l"
1346..1684
/*tag e
/note= "TGF-beta l"
                                                                        Location/Qualiflers
512..1684
/*tag* a
512..598
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 16pp; Japanese.
                          Osteogenetic; tumoricidal; ss.
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599..1684
Human pro-TGF-beta 1 gene
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                                                  TATGATAAAITCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC
                                                                   ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT
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                                                                                                         CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC
                                                                                                                                                            <u>AAGTTAAAAGTGGAGCAGCTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of simian transforming growth factor beta-1 - by cuituring transfected eucaryotic cells, and new precursor proteins, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The cDNA is prepd. from African green monkey cell line BSC-40 expressed in eukaryotic cells in plasmid pSV2. There is 100% between mature similan and human TGF-beta 1. The plasmid also the SV40 promoter and a selection marker, esp. DHFR. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.1%; Score 967.6; DB 9; Length 1560;
llarity 84.9%; Pred. No. 5.8e-186;
Conservative 0; Mismatches 144; Indels 60;
                                       Coding sequence of simian transforming growth factor-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
                                                                growth factor-beta 1; tumour treatment;
                                                                                                                   Location/Qualiflers
261..1433
281..323
7.tag= b
1005..1433
7.tag= c
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                                                                                           Cercopithecus aethiops.
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P-PSDB; AAP80647.
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 25-MAR-2003
09-OCT-1990
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                           GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC
                                          TAIGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC
                                                                                                                                      CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC
                                                                                                                                                     PACCICAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGGGTGGCTGTCCTTTGATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZT, soluble CD4 etc.). (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.1%; Score 967.6; DB 11; Length 84.9%; Pred. No. 5.8e-186; ive 0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1560 BP; 301 A; 547 2; 445 G; 267 T; 0 other;
                                                                                                                                                                 SIV; vaccine; AZT; CD4; cytokines; growth
                                                                                                                                      Simian Transforming growth factor - Betal
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                             ВЪ
                           AAQ03508 standard; DNA; 1560
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/*tag= a
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Matches 1144; Conservative
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                                                                               25-MAR-2003
09-JAN-2003
14-AUG-1990
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                                                                                                                                                                                                          Cebus apella
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1926 TGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAGCTGCCCA 1985
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1017 TCGCCAGCCCCCGAGCCAGGGGAGGTGCCGCCCGGCCGGTGCCCGAGGCCGTGCTCG 1076
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                                                                                                                                                  ACTICCGGAAGGACCTGGGCTGGAAGTGGATCATGAACCCAAGGGCTACCATGCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1806 PORCETCEGEGECCTGCCCTACATTTGGAGCCTGGACAGCAGCAGCAAGGTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1317 GGAGGCTCAAGTTAAAAGTGGAGCAGCAGCTGGGGCTGTACCAGAAATACAGCAACAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          663 GCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACG
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                                          CTCTTTACAACAGTACCCGGGACCGGGTAGCCGGGGAAAGTGTCGAAACCGGAGCCCGAGC
                                                                                                                            CAGAGGCGGACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC
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                                                                                                                                                                                                                                                   macrophage inducible nitric oxide synthase; iNOS; constitutive NOS; interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta; nitric oxide production; hypotension; inflammation; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which has been found to inhibit inducible nitric oxide synthase (1005) gene transcription, esp. in interleakin-1-beta (ILI-beta) stimulated rat smooth muscle cells, and at a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2 (AAR830155) or their active fragments, can be used in the treatment of hypotens.con, such as that associated with severe inflammation or septic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth factor-beta
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                                                                                                                                                                                                              cDNA encoding transforming growth factor-beta 1.
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P-PSDB; AAR83054.
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Search completed: October 9, 2003, 16:12:34 Job time : 446 secs

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Sequence 1, Appli
                                                                                                                   9, 2003, 16:05:13; Search time 100 Seconds (without alignments) 6007.224 Million cell updates/sec
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1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/pcTUS_COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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75-09-620-1320-220
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PCT-US94-03705-3
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US-08-486-057B-3
US-08-470-837-33
US-08-1789-588-3
US-09-123-233-5
US-09-000-069A-1
US-08-868-452-33
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TS-08-470-837-29

TS-08-486-057B-1

US-08-789-588-1

US-09-123-233-1

US-09-169-768-9
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5262319-1
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Maximum Match 10)%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                                                                                      nucleic search, using
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1361
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DB seq length: 2000000000
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Perfect :
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Maximum |
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Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Patent No. 5221620
Patent No. 5168051
Sequence 31, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 254, Appl
Sequence 254, Appl
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5168051-;
Fatent No. 5168051
Fatent No. 5168051
FAPPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
FAPPLICANT: DERYNCK. RIK M.A.; GOEDDEL, DAVID V.
CURNITE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
NUMMER OF SEQUENCES: 2;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 978.8; DB 6;
Pred. No. 3.1e-205;
0; Mismatches 147;
US-09-123-233-11

US-09-123-233-9

US-08-661-753-47

US-08-46-0578-2

US-08-78-258-2

US-09-123-233-3

PCT-US94-03705-4

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US-08-648-11

US-07-668-648-11

US-08-431-333-11

US-08-431-333-11
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US-08-621-803-254
US-09-217-352-254
                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.5%;
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Best Local Similarity 84.8
Matches 1146; Conservative
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us-10-017-372e-36.rni

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491 AAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCGGGCAGAGCTGCGCCCTGCTGAGGCTC
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                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUSTANRE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/O7/669,171
FILING DATE: 19910314
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 5624-159-999
TELEPHONE: 212-790-909
TELEPHONE: 212-790-909
TELEFAX: 212-869-9741
TELEFAX: 212-869-9741
TELEFAX: 1560 DASE DAILS
LENGTH: 1560 DASE PAILS
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                          71.3%; Score 970.8; DB 1;
85.0%; Pred. No. 1.6e-203;
Live 0; Mismatches 142;
STREET: 1155 AVENUE OF THE AMERICAS
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Best Local Similarity 85.0°
Matches 1146; Conservative
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; LOCATION: 261..1430
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               NEW YORK
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                                                  TCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGT
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                                      GGCGCTACCTCAGCAACCGCCTGCTGGCCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG
                                                                                       ATGTCACCGGAGTTGTGCGC CAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07669171
Patent No. 5304541
GENERAL INFORMATION:
APPLICANT: PURCHIO, ANTHONY ?.
APPLICANT: MADISEN, LINDA
APPLICANT: MARNIN, JUNE RAE
APPLICANT: MERMIN, JUNE RAE
TITLE OF INVENTION: TGF-b1/h2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
NUMBER OF SEQUENCES:
ADDRESSEE: PENNIE & EDMONDS
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                               APPLICANI: ma, tungtury
APPLICANI: Wang, Dunrul
APPLICANI: Wang, Zhiwei
APPLICANI: Wang, Zhiwei
APPLICANI: John Tillinghast
APPLICANI: John Tillinghast
APPLICANI: John Tillinghast
APPLICANI: John Tillinghast
APPLICANI: BAGOJE T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: NUMBER: US/09/620,312b
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 220
LENGTH: 2742
LENGTH: 2742
                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.2%; Score 969.4; DB 4; Best Local Similarity 84.8%; Pred. No. 3.6e-203; Matches 1147; Conservative 0; Mismatches 146;
Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
                                                                                                                                                                                                                                                                                                                          ; LOCATION: (842)..(2014)
US-09-620-312D-220
                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (84)
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Patent No. 6569662
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feafyan
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Xee, Aldong J.
APPLICANT: Xee, Aldong J.
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APPLICANT: NICHOLAS M. Dean
APPLICANT: SUSAN F. MUTAS
TITLE OF INVENTION: ANTIESNSE MCDULATION OF TRANSFORMING GROWTH FACTOR BETA
FILE REFERENCE: ISPH-0498
CURRENT PAPLICATION NUMBER: US/(9/661,753
CURRENT FILING DATE: 2000-09-14
EARLIER FILING DATE: 1999-09-17
SEQ ID NOS: 68
SEQ ID NOS: 68
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                TCAGTGCCCACTCCTCCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT
                                                  TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC
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Patent No. 6436909
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; LOCATION: (842)...(2017)
US-09-661-753-28
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                                           Length 2745;
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mark A. Perrella
TITLE OF INVENTION: TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR INHIBITS
TITLE OF INVENTION: SYNTHASE GENE
TITLE OF INVENTION: SYNTHASE GENE
TITLE OF INVENTION: TRANSCR:PTION
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%; Score 965.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 55.2 or 55.8X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reg. No. 34,819
ER: 05433/007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBER: PCT/US94/03705
S April 1994
                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9403705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            3: Fish & Richardson 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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NAME: Janis K. Fraser
REGISTRATION NUMBER: Req.
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         APPLICANT: Mu-En Lee
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02110-2804
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                                    TAGTGCTGACGCCTGCCCGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGG
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              Indels
             Mismatches 147;
2.2e-202;
Pred. No.
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Db 267 ATGCCGCCCTCCGGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGTACTGGTG 326 Oy 71 CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATGGAGCTG 130	OY 131 GTGAAGCGGAAGGGCATCGAGCCATTCGCGGCCAGATCTGTCCAAGCTTCGGCTTGCC 190	9y 191 AGCCCCCGAGGGAGGACGTGCCGCCGGCCGCTGCCTGAGGCAGTACTGGCTCTT 250	OY 251 TACAACAGTACCCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 310	Qy 311 GCGGACTACTACGCCAAGGAGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC 370 i	Oy 371 TATGATAAATTGAAGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 430	Qy 431 CGGGAAGCGCGGAACCTGTATTGCTCTCTCGGCCAGAGCTGCGCTCTCT6AGG 487 I IIII I I I I I I I	Qy 48B CICAAGITAAAAGIGGAGCAGGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG 547 	9y 548 CGCTACCTCAGCAACCGGCTGCTGCCCCAGTGACTCACCGGAGTGCCTTTGAT 607	QY 608 GICACCGGAGTTGTGCGGCAGTGGCTGACCGCAGAGAGCTATAGAGGGTTTTCGCCTC 667	Qy 668 AGTGCCCACTCTTCCTGTGACAGCAAAGATAACACTCCACGTGGAAATTAACGGGTTC 727	0y 728 AATTCTGGCCGGGGGTGACCTGGCCACATCACGCCATGAACGGGCCTTCCTGCTC 787 1 1 1 1 1 1 1 1 1	0y 788 CICATGCCCCCCCCGGGGGGCCCGGCACCTGCACGCTCCCGGCACCCCGGGCC 847	QY 848 CIGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCTGGATACC 907	QY 908 AACTACTGCTTCAGGGGAGAAGAACTGCTGCGGCGGCGCGCTCTACATTGACTTC 967	0y 968 CGGAAGGACTGGGCTGGAAGTGGATTCATGAACCCAAGGGGTACCATGCCAATTTGTGC 1027 1 1 1 1 1 1 1 1 1	Oy 1028 CIGGGCCCTGICCTACAICTGGAGCCTAGACACTCAGTACAGCAGGTCCTGGCTCTG 1087 11	Oy 1088 IACAACCACAACCCGGGGGGGCGCGCGGGGGGCGCGGGGGG
Db 1806 TCTGCCTCGGGCCCTGCTTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGG 1865 Oy 1083 CTCTGTACAACCAGCACACGCGGCGGCGGCGGCGGCGCGTGCTGCGGAGGCGC 1142	Oy 1143 IGGAGCCACTGCCATGGTGTACTACGTGGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCA 1202 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 1203 ACATGATGGTGCTTCCTGCAAGTGCAGGTGCCCGCCCCGCCCCACAGCCCCGCCCA 1262 Db 1986 ACATGATCGTGCGCTCCTGCAAGTGCAGGTCCGGCCCGGCCCGGCCCGGCCCGGCCCGG 2045	Oy 1263 CCCGGCAGCCCGGCCCGCCCGCCTCACCGGGCTGTATTTAAGG 1314	Qy 1315 ACATGGTGCCCCAAGCCCACTTGGGATGGATTAA 1349 L	RESULT 6 US-07-669-171-3	o. 5304541 INFORMATION: CANT: PURCHIO,		CORRESPONDENCE ADDRESS: ADDRESSE: PENNIE & EDWONDS STREET: 1155 AVENUE OF THE AMERICAS	STATE: N.Y. COUNTRY: U.S.A. I DOUGH BOARD BOAR.	COMPUTER: Floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC COMPATIBLE POLOSANDES COMPUTER: Description of the compatible	ACCULTON DATA: ON NUMBER: US/07/669,171 E. 19910314 PATON: A25	ATTORNEY/AGENT INFORMATION: NAME: MISROCK, S. LESLIE REGISTATION UNDHERF. 18.87.	NICATION INFORMATIONE: 212-790-9090	INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1569 base pairs TYPE: MICHEL ACTIVE		67.8%; Score 922.6; DB 1; Length 1569; milarity 83.2%; Pred. No. 5.5e-193; Conservative 0; Mismatches 164; Indels 63: Ga	GGGCCCTTCGGGGCTGCTTCCCGCTGCTGCCGCTGGTGGCTGCT

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546 GGGGCTACCTCAGCAACGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCTTTG 605 [111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
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AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGTGA
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                                                                                  GGCTCAAGTTAAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT
                                                                                                           666 TCAGTGCCCACTCTTCCTCTGACAGCAAGATAACACACTCCACGTGGAAATTAACGGGT
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Patent No. 6436909
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Susan F. Murray
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR FILE REPRENCE: ISPH-0498
CURRENT APPLICATION NUMBER: US/09/661,753
CURRENT FILING DATE: 2000-09-14
EARLIER APPLICATION NUMBER: 60/154,546
EARLIER FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 1
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Pred. No. 2e-176;
3; Mismatches 190; Indels 5
                                                                                                                                                                                                                                                                                1319 CGTGCCCCAAGCCCACTTG3GATCGATTAAA 1349
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Best Local Similarity 80.8%;
Matches 1038; Conservative
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; LOCATION: (868)...(2040)
US-09-661-753-1
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1377 GTCTGGGGCCCTGCCCTACATTTGGAGCCTGGACACACAGTACAGCAAGGTCCTTGCCC 1436
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                                                                              TCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1025
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  --GCCCTGGATA 1256
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                                                     1317 TTAGGAAGGACCTGGGTTGGAAGTGGATCCACGAGGGCCCAAGGGCTACCATGCCAACTTCT
                                                                                                                                   GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
TILLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
GROWTH PRACTOR BETA-2
GROWTH PACTOR BETA-2
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/446,020
FILING DATE: 05-DEC-1989
FRIOR APPLICATION NUMBER: 285,140
FILING DATE: 16-DEC-1988
APPLICATION NUMBER: 234,065
FILING DATE: 18-AUG-1988
APPLICATION NUMBER: 134,065
FILING DATE: 18-AUG-1988
APPLICATION NUMBER: 214,065
FILING DATE: 25-TAN-1988
APPLICATION NUMBER: 106,752
FILING DATE: 25-TAN-1988
FILING DATE: 25-TAN-1989
FILING DATE: 06-OCT-1987
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Pred. No. 3e-160;
0; Mismatches 215; Indels
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Best Local Similarity 78.4%;
Matches 963; Conservative
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                                                                                                                                                 Length 1585;
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.6e-172;
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                                                                                                                                               Score 827.4; Dred. No. 3.6e-0; Mismatches
EARLIER FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 27
LENGTH: 1585
                                                                                                                                              60.8%;
llarity 81.1%;
Conservative
                                                     TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                          ; LOCATION: (413)...(1585)
US-09-661-753-27
                                                                                                                                                          Best Local Similarity
Matches 997; Conserv
                                                                                             NAME/KEY: CDS
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CAGAGGCGGACTACTACGCJAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 365
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                                                                                                                        546 GGCGCTACCTCACCAACCG3CTGCTGGCCCCCCAGTGACTCACCGGAGTGGCTTTTG
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                                   AAATCTATGATAAATTCAA 3GGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG
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                                                  Transforming Growth Factor B Fusion
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                                                                                                                                                                                                                 ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/470,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor
TITLE OF INVENTION: and
TITLE OF INVENTION: And
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 310.2; DB 1
Pred. No. 3.1e-59;
0; Mismatches 18
                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30630-10501
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 3063
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                        CITY: Los Angeles
STATE: California
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Rest Local Similarity
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                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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; LOCATION:
US-08-470-837-29
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
FEATURE:
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                                                                                                                                                                                                          COUNTRY:
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Sequence 29, Application US/08470837
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.

US-08-470-837-29

RESULT 10

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1016 GCCAATITCIGCCIGGGCCCIGICCCIACAICIGGAGCCIAGACACICAGIACAGCAAG 1075
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                                                                                                                                                                                                                                                                                                                        121 GCCAACTTCTGCCTCGGGCCCTGCCCTACATTGGAGCCTGGACACGCAGTACAGCAAG 180
APPLICANT: MCELECLY, NICO
APPLICANT: COX, David
APPLICANT: COX, David
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
APPLICANT: Meyback, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STRRET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STRATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BRA PC COMPALIAL
COMPUTER: PLOADE COMPALIAL
COMPUTER: PLOADE COMPALIAL
COMPUTER: PLOADE COMPALIAL
COMPUTER: PLOADE COMPALIAL
COMPUTER: DATE COMPALIAL
COMPANIES: DATE COMPANIES
COMPUTER: DATE COMPANIES
COMPANIES: DATE COMPANIES
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TELECOMNUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-5116
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/486,057
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
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APPLICATION NUMBER: GB 8927546.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08789588 Patent No. 5922846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cerlett
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Corlett, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Cox, David
APPLICANT: Cox, David
APPLICANT: Schutz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 22.7%; Score 308.6; DB 1; Length Best Local Similarity 94.4%; Sred. No. 6.9e-59; Matches 320; Conservative 0: Mismatches 19; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: BLW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATE:
FILING DATE: 07-JUN 1995
CLASSIFICATION: 514
    PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/521,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION NUMBER: US 07/521,502
FILING DATE: 06-DEC-1999
ATTORNEY AGENT INFORMATION:
NAME: No. 5550494ak, Henry P.
REGISTATION NUMBER: 4-17861/+/Cont3
FELENGUAURICATION INFORMATION:
NAME: No. 5550494ak, Henry P.
REGISTATION NUMBER: 4-17861/+/Cont3
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   Sequence 1, Application US/084860578
Patent No. 555444
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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STATE: New York
COUNTRY: U.S.A.
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1076 GTCCTGGCTCTGTACAACCAAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCTGCTGCGG 1135
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                                                                                                                                                                                                                                                                  141 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
                                                                                                                                                                     Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09169768
Fatent No. 6492508
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
APPLICANT: BROKAN, JANE
APPLICANT: BROKAN, JANE
APPLICANT: APOLELIA, DAVID
ITLEOF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                    Inde ls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1196 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
                                                                                                DB 3;
                                           /product= "human TGF-betal
                                                                                            Score 308.6; DB 3
Pred. No. 6.9c-59;
0; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
IELECOMMUNICATION INFORMATION:
TELEFONE: (516) 228-8484
TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 9:
                                                                                            22.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTĒRISTICS:
LENGTH: 3541 base pairs
TYPE: nucleic acid
STRANUENESS: single
TOPOLOGY: linear
                                                                                                               Hest Local Similarity 94.4
Matches 320; Conservative
                 COLUMNIA 1.336 STATE OTHER INFORMATION: US-09-123-233-1
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       NAME/KEY:
LOCATION:
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                                                                                                Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatib.e
OPERATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
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                                                                                                                                                                                                                                                                               Length 339;
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                                                                                                                                                                                                                                                                             DB 2;
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Best Local Similarity 94.4%; Pred. No. 6.9e-59;
Matches 320; Conservative ); Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
IYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                         US-08-789-588-1
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                                                                                              956 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 1015
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                                    Length 3541;
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                                                          0; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: BONE MORPHOSENETIC PROTEINS AND THEIR TITLE OF INVENTION: USE IN BONE GROWTH FILE REFERENCE: 17972-11 CURRENT APPLICATION NUMBER: US/38/868,452C CURRENT FILING DATE: 1997-06-03 NUMBER OF SEQ ID NOS: 51 SOFTWARE: FASTESQ for Windows Version 3.0 SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                      DB 4;
                                   DB 4;
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                                  Score 308.6; DB 4
Pred. No. 1.1e-58;
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Patent No. 6352972
GENERAL INFORMATION:
                                Query Match 22.7%;
Best Local Similarity 94.4%;
Matches 320; Conservative (
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APPLICANT: Frederick L. Hall
APPLICANT: Lingtao Wu
APPLICANT: BO Han
APPLICANT: Edwin Shors
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Matches 319; Conservative
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US-08-868-452-29
  CDNA
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ORGANISM: Human
, MOLECULE TYPE:
US-09-169-768-9
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NAME/KEY: CDS
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| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1731049 seqs, 1297405648 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appli Sequence 20, App Sequence 28, Appli Sequence 1, Appli Sequence 1, Appli Sequence 19, Appl Sequence 19, Appl Sequence 16, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli 20, Appl 9, Appli 10, Appli 7, Appli 5, Appli Sequence 20, 1 Sequence 9, Al Sequence 10, 2 Sequence 7, Al Description Sequence US-10-087-268-1 US-10-037-270-220 US-10-087-268-4 US-09-948-002-28 US-09-948-002-1 US-09-948-002-1 US-09-948-002-1 US-09-911-904-167 US-09-911-904-167 US-09-911-904-167 US-09-911-904-167 US-09-911-904-167 US-09-911-918-3 US-09-95-458B-9 US-09-95-458B-9 US-09-96-158-10 US-09-96-158-10 US-09-96-158-10 SUMMARIES Query Match Length DB 1821 2742 1821 2745 2094 1585 1376 71.1 71.0 71.0 62.2 66.8 66.8 48.1 18.1 17.6 17.4 16.7 15.4 969.4 9968.2 9658.2 965.8 967.8 967.8 969.4 969.6 969. Score Result Š.

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Gaps

Score 969.8; DB 14; Length 1821; Pred. No. 3e-251; 0; Mismatches 142; Indels 59;

71.3%; 84.9%;

Best Local Similarity 84.9 Matches 1134; Conservative

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Query Match

Sequence 2384, Ap Sequence 11, Appl Sequence 23, Appl Sequence 9, Appl Sequence 9, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 15, Appl Sequence 11, Appl Sequence 6145, Appl Sequence 6145, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 254, Appl Sequence 11, Appl Sequence 1, Appl	linked to a disease or condit
US-10-311-455-2384 US-09-813-271B-11 US-09-913-271B-3 US-09-913-271B-3 US-09-913-271B-3 US-09-913-271B-3 US-09-913-271B-3 US-09-964-761-15319 US-09-864-761-15319 US-09-864-761-15319 US-09-864-761-15319 US-09-864-761-15319 US-09-864-761-15319 US-09-864-761-18644 US-09-813-381-1416 US-09-813-381-1416 US-09-918-95-6145 US-09-918-95-6145 US-09-918-95-6145 US-09-918-95-6145 US-09-918-99-5118644 US-09-918-918-918-918-918-918-918-918-918-91	LIGNMENTS nd polynucleotides 087,268
23381 12 23381 10 4267 10 4267 10 2912 13 2912 10 2912 10 2912 10 2913 10 2913 10 2914 10 1811 10 2914 10 1811 10 1812 8 1822 8 1822 8 1822 8 1822 8 1822 8	SULT 1 Sequence 1. Application US/10087268 Publication No. US20030119010A1 Sequence 1. Application US/10087268 Publication No. US20030119010A1 APPLICANT: Dowell, Elizabeth Ellen APPLICANT: Dowell, Elizabeth Ellen APPLICANT: Powell, Elizabeth Ellen APPLICANT: Dowell, Elizabeth Ellen APPLICANT: Dowell, Elizabeth Ellen APPLICANT: Dowell, Elizabeth Ellen APPLICANT: Dowell, Elizabeth Ellen TITLE OF INVENTION: Polypeptides an FILE REFERENCE: Fibrosis CURRENT FILING DATE: 2002-03-01 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin version 3.1 LENGTH: 1821 TYPE: DNA TYPE:
	pplicat No. US20 No. US20 No. US20 No. US20 No. US20 CE: Fib LCATION CE: Fib LCATION LIMMAN ('UTA LISTION: (51 MATION: 19 MATION: (19 MATION: (19 MATI
8881 8881 8881 8881 8881 8881 841 841 84	RESULT 1 US-10-087-268-1 Sequence 1, Application No. US21 GENERAL INFORMATION APPLICANT: JONSOND APPLICANT: JONSOND APPLICANT: JONSOND APPLICANT: POWELL TILE OF INVENTION FILE REFERENCE: Fil CUNRENT PILLING DATA CURRENT FILLING DATA CURRENT FILLING DATA NUMBER OF SEQ ID N SOCTWARE PATENTION SOCTWARE: PATENTION TYPE: DNA ORGANISM: HUMAN FEATURE: TYPE: DNA ORGANISM: HUMAN FEATURE: CATTON COTHER INFORMATION NAME/KEY: SIG_DEP LOCATION: (512) OTHER INFORMATION NAME/KEY: SIG_DEP LOCATION: (512) OTHER INFORMATION NAME/KEY: SIG_DEP LOCATION: (1685) OTHER INFORMATION NAME/KEY: 3'UTR LOCATION: (1685) OTHER INFORMATION COTHER INFORMATION NAME/KEY: 3'UTR
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TILLE OF INNENTION: No. 0520030104529Alel Nucleic Acids and
TILLE OF INNENTION: No. 0520030104529Alel Nucleic Acids and
FILLE REFERENCE: 784CIP2B.
FILLE REFERENCE: 784CIP2B.
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
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Pred. No. 4.2e-251;
0; Mismatches 146;
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Best Local Similarity 84.8%;
Matches 1147; Conservative
                                                                                                                                                                                                                                               Sequence 220, Application US/10
publication No. US20030104529A1
GENERAL INFORMATION:
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APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Abo, Oing A.
APPLICANT: Xhao, Oing A.
APPLICANT: Xhao, Oing A.
APPLICANT: Xhao, Oing A.
APPLICANT: Xhao, Oing A.
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Jian-Rui
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SOFTWARE: pt_FL_genes Vers
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Ma, Yunqing
Wang, Dunrui
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US-10-037-270-220
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Tillinghast,
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LENGTH: 2742
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                                                                                                                                                                                  APPLICANT: Jonsonn, Julie Ruth
APPLICANT: Jonsonn, Julie Ruth
APPLICANT: Powell, Elizabeth Ellen
TITLE OF INVENTION: Polypeptides and polynucleotides linked
FILE RHEPERCE: Fibrosis
CURRENT APPLICATION NUMBER: US/10/087,268
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 6
SOFWARE: Patentin version 3.1
SEQ ID NO 4
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                                                                       CCCGTGCCCCAAGCCCACCTGGGCCCCCATTAA 2138
             CCCAGGCCCGGCCCCACCCCCCGCCCCCCCT
                                                                                                                                              Sequence 4, Application US/19087268 Publication No. US20030119010A1 GENERAL INFORMATION:
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LOCATION: (1)..(511)

OTHER INFORMATION:

LOCATION: (512).

LOCATION: (512). (1684)

OTHER INFORMATION:

NAME/KET: 814_peptide

LOCATION: (512). (598)

OTHER INFORMATION:
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LOCATION: (1685).
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Sequence 28, Application US/09943002 Publication No. US20030050265Al GENERAL INFORMATION: APPLICANT: Nicholas M. Dean APPLICANT: Susan P. Murray

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1137 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG 1196
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TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-06.07
CURRENT APPLICATION NUMBER: US/09/948,002
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 09/661,753
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/154,546
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 71
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84.6%; Prcd. No. 3.9c-250;
tive 0; Mismatches 147;
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US-09-948-002-28
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ORGANISM: Homo sapiens
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APPLICANT: Chernajovsky, Yuti
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TILLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.1000000
CURRENT APPLICATION NUMBER: US/09/756,283A
CURRENT FILING DATE: 2001.01-09
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
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Sequence 19, Application US/09756283A
Patent No. US20020151478A1
GENERAL INFORMATION:
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APPLICANT: NICHOLAS M. Dean
APPLICANT: Susan F. Murray
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
TITLE OF INVENTION: PACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-0607
CURRENT APPLICATION NUMBER: US/09/948,002
CURRENT FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 71
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Publication No. US20030050265Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                   548 CGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT
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                                                                                                                                                                          TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAAACCGGAGCCCGAGCCAGAG
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                                                                                    Caps
                                                                                     3;
                                                                     Length 1376;
                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 654; DB 10;
Pred. No. 3.2e-166;
(); Mismatches 95;
      TYPE: DNA
OGGANISM: Artificial Sequence
FEATURE:
OTHER OTHER CONSTRUCT;
LOCATION: (1)..(1368)
US-09-756-283A-19
                                                                    Query Match
Best Local Similarity 88.1%;
Matches 724; Conservative 0
                                                                                                                                                                                                                                                                                                                                                         488
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RESULT 8 US-09-756-283A-21 ; Sequence 21, Application US/09756283A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACAGTACCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCGGAGCCAGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATAAATTCAAGGGCACCCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 GGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT---GAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490 CAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 GACGCCTGGCCGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 591.4; DB 10;
Pred. No. 2.3e-149;
0; Mismatches 96;
                  GENERAL INFORMATION:
APPLICANT: Chernajovsky, Yuti
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
ITITE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.1000000
CURRENT APPLICATION NUMBER: US/09/756,283A
CURRENT FILING DATE: 2001.01-09
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PATENTIN version 3.0
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: mIFNbeta-LAP construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.0%;
Matches 662; Conservative (
                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
US20020151478A1
                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)..(1344)
US-09-756-283A-21
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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us-10-017-372e-36.rnpb

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
                          Sequence 1, Application US/09813271B
Patent No. US20020115834A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                     (A) Nico Cerletti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.48;
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 320; Conservative
                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
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                                                                      APPLICANT:
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 RESULT 10
US-09-813-271B-1
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Pred. No. 1.3e-85;
0; Mismatches 32; Indels 52;
APPLICANT: Farr, Spencer B.
APPLICANT: Farr, Spencer B.
APPLICANT: Pickett, Gavin G.
APPLICANT: Weft, Robin Elleen
SPELICANT: Dunn, II, Robert Thomas
TITLE OF INVENTION: CANINE TOXICITY GENES
FILE REFRENCE: 400742000200
CURRENT APPLICATION NUMBER: US/09/911,904
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 386
SOFTWARE: FastSEQ for Windows Version 4.0
SEG ID NO 167
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; Locarion: (1)...(489)
; OTHER INFORMATION: n = A, T, C or G
US-09-911-904-167
                                                                                                    Sequence 167, Application US/09911904
Publication No. US20030096234A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
26.0%;
Best Local Similarity 84.1%;
Matches 445; Conservative
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Canis familiaris
                                                                                     09-911-904-167
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956 TACATIGACITCCGGAAGGACCIGGCIGGAAGISGATICAIGAACCCAAGGGCIACCAI 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
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                                                                                             ADDRESSEE: No. US20020115834Alartis Patent Department
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.7%; Score 308.6; DB 10; Length 339;
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: E. coli LC137/pPLMu.hTGF-betal (DSM 5656)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1..336
COCATION: 1..3306
CTHER INFORMATION: /product= "human TGF-betal"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT AFFICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION NUMBER: US/09/813,271B
FILING DATE: 12-Mar-2001
FILING DATE: 12-Mal-95
APPLICATION NUMBER: EPP 94810439.3
FILING DATE: 25-Mal-94
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REFERENCE/DOCKET NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
     production
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.6e-73;
TITLE OF INVENTION: New process for the biologically active
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1013
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                                                                                                                                                                                                                                           774 GGCCCTTCCTGCTCCTCATGGCCACCCGCTGGAGGGCCCAGCACCTGCACAGCTCCC 833
                                                       714 AAATTAACGGGTTCAATTCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACC 773
                               CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT 659
                                                                                                   660 TTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACA-----CACTCCACGTGG 713
                                                                                                                                    915 TAGAAATCAGCATTCACTGTCCATGTCACCTTTCAGCCCAATGGAGATATCCTGGAAA 974
795 CCAAACAGCGCIATATCGGTGGCAAGAATCTGCCCACGGGGCACTGCCGAGTGGCTGT 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCAGGCGCTGGAGCCATGCTGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGC
                                                                                                                                                                                                                                                                                                                GGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTC
                                                                                                                                                                                                                                                                                                                                                 TCIACATIGACTICCGGAAGGACCTGGGCTGGAAGTGGATICATGAACCCAAGGGCTACC
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/10028158
Publication No. US20020110833A1
GENERAL INFORMATION:
APPLICANT: Caniggia, Isabella
APPLICANT: Caniggia, Isabella
APPLICANT: Lye, Stephen
TILE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TILLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TILLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TILLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TILLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TILLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
PRIOR RAPLICATION NUMBER: US/09/380,662
PRIOR APPLICATION NUMBER: PCT/CA98/00180
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
SUFFRMER OF SEQ IN NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1194 AGCTGTCCAACAIGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGC 1242
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 20
LENGTH: 2574
                                                                                                                                                                                                          975
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                                                                                                                                                                                          Sequence 3. Application US/09906158
Sequence 3. Application US/09906158
PUBLICATION NO. US20030078217A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESS CURRENT APPLICATION NUMBER: US/09/906,158
CURRENT APPLICATION NUMBER: US/09/906,158
CURRENT FILING DATE: 2001-07-14
           440
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                                                                                 .196 CTGTCCAACATGATCGTGC3TTCCTGCAAGTGCAGCTGA 1234
                                                                                                   Score 245.8; DB 11;
Pred. No. 3.3e-56;
3; Mismatches 532;
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Best Local Similarity 53.3%;
Matches 666; Conservative
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LOCATION: (254)...(1492)
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ORGANISM: Homo sapiens
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LENGTH: 2574
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OTHER INFORMATION: Vector for transforming supporting cell with a foreign to OTHER INFORMATION: a gene product of interest
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                                                                           134 CGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGC 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT TRANSPORTION TO THE REPERENCE: Chen, Una TITLE OF INVENTION: Method for growing stem cells FILE REPERENCE: P665670S0 CURRENT EMPLICATION NUMBER: US/09/957,458B CURRENT FILING DATE: 2001-09-21 PRIOR APPLICATION NUMBER: EP 99116533 PRIOR FILING DATE: 1999-08-24 NUMBER FILING DATE: 1999-08-24 NUMBER PETING PATE PRIOR FILING DATE: 1999-08-24 SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09957458B Publication No. US20030166271A1 GENERAL INFORMATION:
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                                                                                                                                                Length 2574;
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Pred. No. 3.3e-56;
[; Mismatches 532
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Llarity 53.3%;
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; LOCATION: (254)..(1492)
US-10-028-158-20
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                                                                                                                                                                                          36 IGCCGCIGCTGCTGCTGCTGTGGCTGCTASIGCTGACGCCTGGCCGGCCGGCCGCCGCCG
                                                                                                                                                                Gaps
                                                                                                                                                              45;
                                                                                                                                DB 11; Length 2879;
                                                                                                                                                              Indels
                                                                                                                                                            0; Mismatches 541;
                                                                                                                                Score 236.4; DB 1 Pred. No. 1.1e-53;
                                                                                                                                17.4%;
52.8%;
                                                                                                                                              Best Local Similarity 52.8
Matches 656; Conservative
                                                                                       ; LOCATION: (611)...(1843)
US-09-906-158-10
SEQ ID NO 10
LENGTH: 2879
TYPE: DNA
ORGANISM: Mus musculus
                                                                       NAME/KEY: CDS
LOCATION: (61)
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Best Local
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APPLICANT: Brans M. Freier
TITLE OF INVENTION ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
FILE REFERENCE: RTS-0257
CURRENT APPLICATION WHBER: US,09/906,158
CURRENT FILLING DATE: 2001-07-14
NUMBER OF SEQ ID NOS: 168
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                               809 AATGAACTGGCCGTCTGCCCCAAAGGAATTACCTCTAAGGTTTTTCGTTTCAATGTGTCC
                                                                                                                    -----AGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAA
                                                                                                                                             929 AACCCCAGCTCCAAGCGCAJAGAGCAGAGAATTGAGCTCTTCCAGATACTTCGACCGGAT
                                                                                                                                                                                               GAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCT
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   371 TATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC
                                                           CGGGAAGCGGTGCCGGAACTTGTTTGTTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC
                                                                                       869 TCAGIGGAGAAAAIGGAACCAATCIGIICCGGGCAGAGIICCGGGICIIGCGGGIGCCC
                                                                                                                                                                              530 TACAGCAATGATTCCTGGGGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCG
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US-09-906-158-10
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ADDRESSEE: No. US20020115834Alartis Patent Department
STREET: 564 Morris Avenue
CITY: Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (A) Nico Cerletti
TITLE OF INVENTION: New process for the production of
biologically active protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: E. coli LC137/pPLMu.TGF-betal(44/45)beta3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc - "recombinant hybrid DNA of
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                               PRIOR METELLATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: PEO 94810439.3
APPLICATION NUMBER: PEO 94810439.3
FILING DATE: 25-Jul-94
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22640
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 32-6940
TELECOMMUNICATION OF 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-3001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09813271B Patent No. US20020115834A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 336;
                                                                                                                                                                                                                                                                      LOCATION: 1.336
OTHER INFORMATION: /product~ "hybrid TGF-beta named
NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product* "N-terminal 44 amino
acids of human TGF-betal"
                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 16.7%; Score 227.2; DB 10; Length Best Local Similarity 79.8%; Pred. No. 2.1e-51; Matches 268; Conservative 0; Mismatches 68; Indels
                                                                                                                        NAME/KEY: mat_peptide
LOCATION: 133..38
OCHER INFORMATION: /product- "C-terminal 68
acids of human TGF-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1196 CIGICCAACAIGAICGIGCGIICCIGCAAGIGCAGC 1231
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                                                                                                                                                                                                                                                                                                                          TGF-betal-3" SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                   NAME/KEY: CDS
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Sequence:

Run on:

Searched:

Database

Result No.

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BIS86959 603313837
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BM0572677 AGENCOURT
BX11243 BX412434
CA25775 UI.HFEI-
BM02192 AGENCOURT
BUG33535 UI.H-FEI-
BG50488 60244826
BUG33922 UI.H-FEI-
BUG33922 UI.H-FEI-
BUG33537 UI.H-FEI-
BUG33922 UI.H-FEI-
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BX34425 BX444425
BX53462 AGENCOURT
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B1195242 G02444518
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BQ0544518
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BX325288
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AI743724 wg53b06.x
BG683840 602651694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12768 row: h column: 08
High quality sequence start: 9
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BM562135
                                                        BM562135 AGENCOURT
BX355682 BX355682
BX349319 BX349319
BX335351 BX335351
                                                                                                                                             (without alignments)
10285.570 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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High quality sequence stop: 647.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Emall: seqreféqenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9160.r For
more information about this cluster, sec
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cgi-bin/cluster.cgi?seq-CSODI002CE03NPl&cluster-9160.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI002CE03NPl.
Location/Qualifiers
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847 CCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATAC
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/mol_type-"mRNA"
/db_xrefr"taxon:9606"
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Contact: Genoscope

Genoscope - Centre National de Sequencaqe

Genoscope - Centre National de Sequencaqe

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9160.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bh/cluster.cgi?seq-CSOBAQCSSDBQ4_CSO5596_1scluster-9160.r.

Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSOBAGO592D04_CSO5596_1.

Location/Qualifiers

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1. 906
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COT 25-NORMALIZED
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 900)
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/mol type="mRNA"
/do_zref="taxon:9606"
/clone="CSOEL107107"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORWALIZED"
/cell_the="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORWALIZED"
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8X343319 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMA
Homo sapiens CDNA clone CSODL010YL07 5-PRIME, MRNA sequence-
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  DB 13;
Score 698.4; DB 13;
Pred. No. 3.3e-142;
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al Similarity 81.9%;
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                                                                           /tissue_type-*PlACENTA COT 25-NORMALIZED"
/close_lib-*fomo saptens PlACENTA COT 25-NORMALIZED"
/note-*list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Nor I and cloned into the Not I and Ecok V
sites of the pCMYSDORT 6 vector. Library was normalized."
280 c 323 g 203 t
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            /organism."Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSODI013YH16"
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BP 191 91006 EVHY cedex - France
BRail: seqrefégenscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies. Por
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=cS0D1013DD08NPl
bttp://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=cS0D1013DD08NPl
cscluster=9160.r. Contact: Feng Liang Email: fliang@lifetech.com
0RL: http://tullength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0D1013DD08NPl.
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 983)
                                                                                                                                                                                           CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC
                                                                                AAATCTATGATAAATTCAAG GGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG
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 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC
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Full-length CDNA libraries and normalization
Unpublished
Contact: Genoscope
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Oy 399 GCTTAIATATGCTGTTCAACACGTGGGGAGGGGTGGCGGAACCTGTATTGC 458	Oy 578 AGTGACTCACCGGAGTGCTGTCTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACC 637	QY 698 AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCGGGTGACCTGGCCACC 757 Db 607 AACACACTGCAAGTGGACATCAACGGGTTCACTGGCCGCGCGGGGTGACCTGGCCACC 548 QY 758 ATTCACGGCATGAACGGCCCTTCCTGCTCCTCATGGCCACCCGCTGGAGAGGCCCAG 817 IIII	0y 818 CACCTGCACAGCTCCGGCACCGCGAGCCTGGATACCAACAGCTACCCATACGACGGG 877	998 GAACCCAAGGCTACCATGCCAATTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAA 11 11 11 11 11 11 11 11	Db 180 AAGCCCAAGGTGGACCACCACCATGATCGTGCCTCCTGCAAGTGCAGGTGTAGGT 121 Qy 1238 CCGGCCCGCCCAAGCCCGCCCACCCGGCAGCCGCCCCACCCCGCCCGCCCCGCCGCCGCCGCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGAGCCCGAGCCCGAGCCCAATAA 1 bb 60 TTGCCCATGGGGGCTGTATTTAAGGACCCGCCCCCAAGCCCAAGCCCAATAA 1	RESULT 6 BX434425/C LOCUS BX434425 DEFINITION BX434425 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE014YE16 ACCESSION BX434425 GI:30779291 KEYWORDS EST. 15-MAY-2003 BX434425 GI:30779291
0y 1118 GCGCCGTGCTGCTGCCGCAGGCCCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC 1177 1 1 1 1 1 1 1 1	1298 CGGGCTG 1305 12		ţ Ç	TWOILTOGEN. THIS Sequence belongs to sequence cluster 910U.F FOR more information about this cluster, see http://www.genoscope.cns.fr/ eq:-bh/cluster.cg1?seq=CSOACO24DB10NP2.cluster=9160.r. Contact :	Once-1st Strand Cuba Was primed With a NOLI-011go(dI) primer. Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized." BASE COUNT 176 a 283 c 346 g 219 t 17 others ORIGIN OUETY MATCH 47.5%; Score 646; DB 13; Length 1041; Best Local Similarity 80.4%; Pred. No. 8.8e-131; MATCHES 868; Conservative 10; Mismatches 135; Indels 67; Gaps 8;	Oy 279 GGGAAGTGTCGAACCGGAGCCGAGGCGACTACTACGCCAAGGGGCACCC 338

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1043 bp mRNA lincar EST 20-FFB-2002
AGENCOURT_6544437 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5550039
5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1043)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Site 1: Not1: Site_2: Sal1; Cloned unidirectionally;
Oligo-dI primed. Average insert size 1.767 kD. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
                                                                                      CGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGC
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                              Email: crapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can http://image.llni.gov
Plate: LiaM12261 row: i column: 16
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Location/Qualifiers
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/mol_type="mRNA"
/mol_type="mRNA"
/do_tref="texton:9606"
/done="CSODEGI4YEL6"
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BP 191 91006 EVRY cedex - France
BRAIL: seqrefégenoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9160.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgibin/cluster.cgi7seq=CSOBARO18ABBORN18cluster=9160.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBARO28ABORNIL.
Location/Oualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                           1 (bases 1 to 888)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
   sapiens (human)
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                                                                      396 ACAGCTTATATATGCTGTT:AACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTAT
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                           Score 607; DB 12; Length 1 Pred. No. 2.9e-122; ); Mismatches 122; Indels
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/cell_type="HELA"
/clone="lib="HELA"
/clone="lib="Hend cDNA was primed with a NotI-oligo(dT)
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digested with Not I and cloned into the Not I and EcoR V
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length, CDNA libraries and normalization
      BX383773 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CONA clone CSODKOO1YA15 3-PRIME, MRNA sequence.
BX383773
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cgj.bin/cluster.cgi?seq-cSODK001AA08Np1&cluster-9160.r. Contact
cgj.bin/cluster.cgi?seq-CSODK001AA08Np1&cluster-9160.r. Contact
Feng Liang Email : fliang & Lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODK001AA08NP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9160.r
more information about this cluster, see
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Genoscope - Centre National de Sequencage
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/clone=lb-"Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED
/clone=lb-"Homo sapiens neurolady dubble strand cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcw/NSPORT 6 vector. Library was normalized."

79 a 272 c 257 g 148 t 3 others
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                                                                                                                                                                                                                    Length 859;
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                                                                                                                                                                                                                 Score 577.4; DB 9;
Pred. No. 8e-116;
2; Mismatches 93;
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AL530081.2 GI:31067916
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BP 191 91006 EVRY cedax - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Mas normalized. Library was constructed by Life Technologies, a
division of Invitrogen This sequence belongs to sequence cluster
9160.r For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Feng Liang Email : fliang@lifetech.com URL :
http://fblllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD009BG03QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              CGGCCTTTCCTGCTTCTCATGGCACCCGCTGGAGGGCCCAGCATCTGCAAAGCTCC
                                                                                           CGGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCT
                                                                                                                                                                       CTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTAC
                                                                                                                                                                                                                                     GACATCAACGGGTTTACTACJGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAAC
                             CGGCCCTTCCTGCTCCTCAT3GCCACCCCGCTGGAGGGCCCCAGCACCTGCACAGCTCC
                                                                                                                         CTGGCCCTGGATACCAACTACTGCTTCAGCTCCACGAGAAGAACTGCTGCGGCGCAG
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replace
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AUTHORS
TITLE
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ACCESSION VERSION KEYWORDS SOURCE

FEATURES

RESULT 9 AL530081

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//do_hos="DH10B (phage-resistant)"
//do_hos="DH10B (phage-resistant) / do_hos="DH10B (phage-r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE260971 717 bp mRNA linear EST 26-OCT-2000 601153715F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509931 5',
                     555 TCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCTTTGATGTCACCG 614
                                                                                                                                                                                                                                                                                                         675 ACTITICITICACAGCAAAGATAACACACTICACGTGGAAATTAACGGGTTCAATTICTG 734
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammaiian Gene Collection (MGC)
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                                                                                                                                                                                                                                  615 GAGTTGTGCGGCAGTGGCTGACCCGCAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                             GCCGCCGGGGTGACCTGGCCACATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGC
TAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 713.
Location/Qualifiers
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BE260971
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BE260971
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BE312000 713 bp mRNA linear EST 26-OCT-2000 601154768Fl NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3510592 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: AVCC
CDNA Library Prepararion: Ling Hong/Rubin Laboratory
CDNA Library Prepararion: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM195 row: h column: 17
High quality sequence start: 2
High quality sequence stop: 713.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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87.5%; Pred. No. 2.3e-114;
Live ('; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                 Unpublished
Contact: Robert Straumberg, Ph.D.
                                                                                                 BE312000.1 GI:9130123
                                                                                                                                                       Homo sapiens (human)
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                                                   mRNA sequence.
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Score 562.6; DB 10; Pred. No. 1.3e-112; 41.38; Query Match Best Local Similarity

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/cissue_type="epidermoid carcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/lab_host="NHH_MCS_102"
/clone_lib="NHH_MCS_102"
/note="Organ: salivary gland; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dI priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHH_MGC Library."

7 a 292 c 255 g 161 t
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Clone distribution: MGC clone distribution info found through the I.M.A.G.E. Consortium/LLNL at: http://mage.lnl.gov
Plate: LLCM2375 row: c column: 22
High quality sequence stop: 599.
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86.7%; Pred. No. 1.9e-112;
tive 0; Mismatches 95;
                                                                                                                       /organism="Homo sapiens"
                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6211917"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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     Indels
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     Mismatches
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Contact: Robert Strausberg, Ph.D.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0bb009YM06"
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Mammalia; Eutheria; P.:imates; Catarrhini; Hominidae; Homo.

    (bases 1 to 925)

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Tissue Procurement: Life Technologies, Inc.
CDNA Library Prepara:Lon: Life Technologies, Inc.
CDNA Library Prepara:Lon: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11444 row n column: 02
High quality sequence stop: 874.
Location/Quailfiers
I. 925
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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//db_tref="taxon:9606"
/clone="!HAGE:5178433"
/lab_host="DH108"
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Homo sapiens
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JOURNAL
COMMENT
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BI818841
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Name list Eutheria; Chordata; Craniata; Vortebrata; Euteleostomi; Bukaryota; Matazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1. (Bases I to 841)

E. 11. (Bases I to 841)

E. 11. (Bases I to 841)

Full:length cDNA libraries and normalization

On Feb 13, 2001 this sequence version replaced gi:12793573.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: Segref(@genoscope.cns.fr, Web: www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

plio.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/Cluster.cgi?seq-cSODD009BG03NP1&cluster=9160.r. Contact:

Feng Liang Email: fliang@lifetech.com URL:

Feng Liang Email: fliang@lifetech.com URL:

Location/Cualifiers

Location/Cualifiers
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                                                                                                                                                                                                                                                                                                                                              485
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/tissue_type="NEUROBLASTOWA COT 50-NORMALIZED"
/clone_lib-"Homo sapiens NEUROBLASTOWA COT 50-NORMALIZED"
/note="list strand cDNA was prined with a NotI-oilgo(dI)
priner. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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                                                                                                                                 566 ACCICCGAGAAGCGGIACCIGAACCCGIGIIGCTCICCCGGGCAGAGCIGCGICIGCTGA
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                                                                                                                                              <u> AGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGA</u>
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                                                                       CGGTGCCGGAACCTGTATTGCTCT-CTCGGGCAGAGCTGCGCCCTGCTGAGGTCAAGTTA
                                                     Gaps
                                                     57;
                                   Length 841;
                                                    Indels
                                   Score 521.8; DB 9;
Pred. No. 1.1e-103;
8; Mismatches 106;
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B1084718 956 bp mRNA linear EST 20-JUN-2001 602869722T1 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:5014421 3',

LOCUS

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3 SAACCGIGTTGGCTCTTCCCGGGGAAGAGCTGCCGTCTGCGGGGCTCAAGTTAAAAGT 776
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                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 956) NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                Email: cgapDs-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA821 row: 1 column: 06
High quality sequence start: 3
High quality sequence stop: 793.
Location/Qualifiers
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                                                                                                                                                                                                                                                                      Unpublished
Contact: Robert Strausberg, Ph.D.
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BI084718.1 GI:14503048
                                                                                                Homo sapiens (human)
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